

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-896 <RES>
 A:Cross-references: GB:S79263; NID:q1086954; PID:AA835068.1; PID:q1086955
 C:Genetics:
 C:Gene: rtl-3Rbeta
 C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology
 C:Keywords: cytokine receptor
 F:39-235/Domain: cytokine receptor homology <CRS1>
 F:253-433/Domain: cytokine receptor homology <CRS2>
 I56563 Length: 896 July 16, 2003 13:42 Type: P Check: 5352 ..
 Found using 'var2' (kam816.key)

421 PEYKGLMSEMSNECTWTDTDMVMTLWIVLIVFLITFLALRFGCIYCKLIRKREKI |-----|
 471 477

481 PMSKSLFQDGGKGLMPGSGTVTFSSKNPTPGPQNNLFSELQVS

 1 match found in sequence:
 S36348 ; TOIG of: s36348 check: 3344 from: 1 to: 234
 (from "var2pir.pep")
 TOIG of: s36348 check: 3344 from: 1 to: 234

F1:S36348 - opacity protein opa65 - Neisseria gonorrhoeae (strain VP1)
 (fragment)
 N:Alternate names: outer membrane protein opa65
 C:Species: Neisseria gonorrhoeae
 A:Variety: strain VP1
 C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
 C:Accession: S36348; S28617
 R:Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
 EMBO J. 12, 641-650, 1993
 A:Title: Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial
 cells.
 A:Reference number: S36328; MUID:93178439; PMID:8440254
 A:Accession: S36348
 A:Molecule type: DNA
 A:Residues: 1-234 <KUP>
 A:Cross-references: EMBL:Z18940; NID:g49336; PID:CAA79373.1; PID:g940802
 A:Experimental source: strain VP1
 A:Note: expression of opacity proteins is regulated by the number of translated
 repeat elements CTCGT, which code for part of the signal sequence; the protein
 can only be synthesized when the number of repeats place the start codon in
 frame with the rest of the protein
 C:Genetics:
 A:Gene: opa65
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-234/Product: opacity protein opa65 #status predicted <MAT>
 F:11-19/Domain: transmembrane #status predicted <TM1>
 F:20-51/Domain: extracellular #status predicted <EXT1>
 F:28-37/Region: semivariable region
 F:52-60/Domain: transmembrane #status predicted <TM2>
 F:65-71/Domain: transmembrane #status predicted <TM3>
 F:72-107/Domain: extracellular #status predicted <EXT2>
 F:78-107/Region: hypervariable region HV1
 F:108-122/Domain: transmembrane #status predicted <TM4>
 F:128-138/Domain: transmembrane #status predicted <TM5>
 F:139-185/Domain: extracellular #status predicted <EXT3>
 F:144-176/Region: hypervariable region HV2
 F:186-198/Domain: transmembrane #status predicted <TM6>
 F:202-210/Domain: transmembrane #status predicted <TM7>
 F:211-225/Domain: extracellular #status predicted <EXT4>
 F:226-234/Domain: transmembrane #status predicted <TM8>

S36348 Length: 234 July 16, 2003 13:42 Type: P Check: 3344 ..
 Found using 'var2' (kam816.key)

22 ITHDYPEPTGAKKAQLSTVSDYFRNIRTHSIHPRVSGYDFGWRILADYARAKWRESN |-----|
 82 SSKKVTEDIDKNKREKTEHENGSTHVASSLGLSTIYDFQISDKI 72 78

--- Search Statistics ---

| Times: | CPU | Total Elapsed |
|--------|-------------|---------------|
| | 00:00:00.00 | 00:00:01.00 |

| | |
|--------------------------------|---|
| Number of sequences searched: | 4 |
| Number of sequence hits: | 4 |
| Number of separate matches: | 0 |
| Number of sequence hits saved: | 0 |

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01 10 Intelligenetics
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Release 5.4

-- Outline of search "var2_plr" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.

Selected sequence key from "kam816.key":

var2 (AA) ID var2 AA preliminary pattern

1 followed by

2 a or k or g

2 1 or r

2 y

2 k or r or h

2 k or r or h

2 wk

Selected files:

File : var2plr.pep

-- Output Parameters --

| Format Options: | File Options: |
|-----------------------------|---------------|
| Nucleic acid code matching | Exact |
| Find non-matching hits only | No |
| Report key used | Yes |
| Note position of hit | Yes |
| Display full annotations | Yes |
| Sequence context | 50 |

-- Run Parameters --

| Run mode | Batch |
|--------------------------|-------|
| Time to start comparison | now |
| Notify at end of run | No |

1 match found in sequence:

b64300 ; TOIG of: b64300 check: 316 from: 1 to: 243

(from "var2plr.pep")

TOIG of: b64300 check: 316 from: 1 to: 243

P1:B64300 - hypothetical protein MJ0002 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: B64300

R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.A.; Fitzgerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reisch, C.I.; Overbeek, R.;

Georgiades, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.;

Georgiades, N.S.M.; Weidman, J.F.; Fuhmann, J.L.; Nguyen, D.; Uterbeck, T.R.;

Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.;

Woose, C.R.; Venter, J.C.

A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.

A:Reference number: A64300; MUID:96337999; PMID:8688087

A:Accession: B64300

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-243 <BUL>

A:Cross-references: GB:067459; GB:L77117; MID:92826236; PIDN:AAB97989.1;

PID:q1498759; TIGR:MJ0002

C:Genetics:

A:Map position: REV4071-3340

B64300 Length: 243 July 16, 2003 13:42 Type: P Check: 316 ..
Found using 'var2' (kam816.key)

62 DVSFELGKFLRELLKPNANFETALSDKVLSSKHYEDVKGIAVNCICKKLYHMKGFA
112 118

122 KPLQCKEKESYNPNKTLTYLRAYOGILCLESSEKSFSSRCL

1 match found in sequence:
c83557 ; TOIG of: c83557 check: 491 from: 1 to: 212

(from "var2plr.pep")

TOIG of: c83557 check: 491 from: 1 to: 212

P1:C83557 - chloramphenicol acetyltransferase PA0706 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: C83557

R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brinkman, F.S.L.; Hutnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R.L.; Goltz, L.; Tolentino, E.; Westbrook-Wadman, S.; Yuan, Y.; Brody, L.L.;

Coulter, S.N.; Folger, K.R.; Kas, A.; Lardly, K.; Lim, R.M.; Smith, K.A.;

Spencer, D.H.; Wong, G.K.S.; Wu, Z.; Paulsen, I.T.; Reizer, J.; Sauter, M.H.;

Hancock, R.E.W.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.

A:Reference number: A62950; MUID:20437337; PMID:10984043

A:Accession: C83557

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-212 <STO>

A:Cross-references: GB:AE004506; GB:AE004091; MID:9946584; PIDN:AG04095.1;

GSDB:G00131; PASP:PA0706

A:Experimental source: strain PA01

C:Genetics:

A:Gene: cat: PA0706

C:Superfamily: Agrobacterium chloramphenicol acetyltransferase

C83557 Length: 212 July 16, 2003 13:42 Type: P Check: 491 ..

Found using 'var2' (kam816.key)

...

150 VAIVGNPARIKRFSDGDIQNLLEAMWMDPLDIEAMPLCTGDPILRYHMKRO
200 206

210 ATA

1 match found in sequence:

156563 ; TOIG of: 156563 check: 5352 from: 1 to: 896

(from "var2plr.pep")

TOIG of: 156563 check: 5352 from: 1 to: 896

P1:I56563 - interleukin-3 receptor beta-subunit - rat

C:Species: Rattus sp. (rat)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999

C:Accession: I56563

R:Appel, K.; Buttini, M.; Sauter, A.; Gebicke-Haerter, P.J.

J. Neurosci. 15, 5800-5809, 1995

A>Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured

microglia and its mRNA expression in vivo.

A:Reference number: 156563; MUID:95370942; PMID:7643220

A:Accession: I56563

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-- Outline of search "varl_pir" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.

Selected sequence key from "kam816.key":

```
varl (AA) ID varl AA preliminary pattern
1 followed by
2 a or k or g
2 l or r
2 y
2 k or r or h
2 k or r or h
2 f
2 k or r or h
```

Selected files:

File : varlpir.pep

-- Output Parameters --

| Format Options: | File Options: |
|-----------------------------|----------------------|
| Nucleic acid code matching | Exact |
| Find non-matching hits only | Indirect file |
| Report key used | Sequence or key file |
| Note position of hit | List of hits |
| Display full annotations | Hit display |
| Sequence context | Name and annotations |
| | 50 |
| | Yes |
| | Yes |
| | Yes |

-- Run Parameters --

| Run mode | Batch |
|--------------------------|-------|
| Time to start comparison | now |
| Notify at end of run | No |

1 match found in sequence:

a71219 : TOIG of: a71219 check: 5893 from: 1 to: 269
(from "varlpir.pep")

TOIG of: a71219 check: 5893 from: 1 to: 269

P1:A71219 - hypothetical protein PH0012 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii

C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000

C:Accession: A71219

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.; Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.; Nakazawa, H.; Takamiya, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.; Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3.

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: A71219

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-269 <KAM>

A:Cross-references: GB:AP000001; NID:g3236128; PIDN:BAA29080.1; PID:g3256397

A:Experimental source: strain OT3

A>Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH0012

A71219 Length: 269 July 16, 2003 13:37 Type: P Check: 5893
Found using 'varl' (kam816.key)

63 FYNQAMIGLMGVKAYQRRGIGTEVFRLLIEIGRRKVDITRLDASSQGYLKKFQVD
113 119

123 EYTRRYELMERPIKRVGEVENVKIPNMVKEIDKKAFGDDRIVLE

1 match found in sequence:
b70452 : TOIG of: b70452 check: 9383 from: 1 to: 257
(from "varlpir.pep")
TOIG of: b70452 check: 9383 from: 1 to: 257

P1:B70452 - conserved hypothetical protein aq_1768 - Aquifex aeolicus

C:Species: Aquifex aeolicus

C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999

C:Accession: B70452

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Sneed, M.A.; Keller, M.; Anjlay, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V.

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: B70452

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-257 <AQF>

A:Cross-references: GB:AE000755; NID:g2984063; PIDN:AAC07614.1; PID:g2984074; GB:AE000657

A:Experimental source: strain VF5

C:Genetics:

A:Gene: aq_1768

B70452 Length: 257 July 16, 2003 13:37 Type: P Check: 9383
Found using 'varl' (kam816.key)

94 CIPENVYLVKVSINPRDTRKLSKRVRELYLALPLVKAICYEIKPEYNNKLYRKRRNIN
144 150

154 KMMTHFYKLLIERVKECGVEVVDKTOPSPNFGEDVIFETEAERN

1 match found in sequence:

e71510 : TOIG of: e71510 check: 2099 from: 1 to: 696
(from "varlpir.pep")

TOIG of: e71510 check: 2099 from: 1 to: 696

P1:E71510 - probable oligopeptide binding lipoprotein - Chlamydia trachomatis (serotype D, strain TW3/Cx)

C:Species: Chlamydia trachomatis

C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999

C:Accession: E71510

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, W.P.; Olinger, L.; Tatusov, R.L.; Zhao, Q.; Koonin, E.V.; Davis, R.W. Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.

A:Reference number: A71570; MUID:99008009; PMID:9784136

A:Accession: E71510

A>Status: preliminary

```

A:Molecule type: DNA
A:Residues: 1-696 <ARN>
A:Cross-references: GB:AE001321; GB:AE001273; NID:93328906; PIDN:AA068080.1;
PID:93328915
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: opvA_4

E71510 Length: 696 July 16, 2003 13:37 Type: P Check: 2099
Found using 'varl' (kam816.key)

576 LGTPEDRALHMSGALKEKGSANAVGSCNEADRIIEQLSEYEDSNKROALYHREHVI
1-----1
626 632

636 HESPYAFLYSRQSLVLYKEFYKNIFVPTHEQDLIPGAODETVNLISM

1 match found in sequence:
964502 : TOIG of: 964502 check: 5094 from: 1 to: 765
(from "varlpir.pep")
TOIG of: 964502 check: 5094 from: 1 to: 765

P1:G64502 - hypothetical protein MJ1626 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999
C:Accession: G64502
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton,
G.G.; Blake, J.A.; Fitzgerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage,
A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.;
Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.;
Georgiades, N.S.M.; Weidman, J.F.; Fuhmann, J.L.; Nguyen, D.; Dillerback, T.R.;
Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts,
K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.;
Moese, C.R.; Venter, J.C.
A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: G64502
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-765 <BUL>
A:Cross-references: GB:U67602; GB:L77117; NID:91592214; PIDN:AA09649.1;
PID:91500524; TIGR:MJ1626
C:Genetics:
A:Map position: REV1602382-1600085

G64502 Length: 765 July 16, 2003 13:37 Type: P Check: 5094
Found using 'varl' (kam816.key)

230 ILANKYSEKDERELITLILNIYDSLTDQKILRGHLSVLLGDEDEKRIYFKOLF
1-----1
280 286

290 EKLDPALSDQIKSLKSHGKTLITLRINIKLPANFYNREFLK

1 match found in sequence:
997093 : TOIG of: 997093 check: 8978 from: 1 to: 181
(from "varlpir.pep")
TOIG of: 997093 check: 8978 from: 1 to: 181

P1:G97093 - glutathione peroxidase [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: G97093
R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, O.; Gidson,
R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hittl, J.; Wolf, Y.I.; Tatuov, R.L.;
Sabathe, F.; Doucelte-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.;
Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing
Bacterium Clostridium acetobutylicum.
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: G97093
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-181 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK79538.1; PID:915024524; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1571
C:Superfamily: glutathione peroxidase

G97093 Length: 181 July 16, 2003 13:37 Type: P Check: 8978
Found using 'varl' (kam816.key)

1 MSIDYFKVDINGEDISMEEYRGKALLIVNTASKCGFTPOYEDLEALYKFKGFGEVIG
1-----1
46 52

61 FPCNPFENQEPGTRNDIKFKCQINQVTRKIPDKVDVNGENE

1 match found in sequence:
qdbp91 : TOIG of: qdbp91 check: 89 from: 1 to: 183
(from "varlpir.pep")
TOIG of: qdbp91 check: 89 from: 1 to: 183

P1:Q0BP9L - gnt protein - phage lambda
C:Species: phage lambda
C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 17-Jul-1998
C:Accession: I43010; C43016; H93737; A04387
R:Daniels, D.
Submitted to the Nucleic Acid Sequence Database, September 1982
A:Reference number: A94614
A:Accession: I43010
A:Molecule type: DNA
A:Residues: 1-183 <DAN>
R:Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.
J. Mol. Biol. 162, 729-773, 1982
A>Title: Nucleotide sequence of bacteriophage lambda DNA.
A:Reference number: A92891; MUID:83189071; PMID:6221115
A:Accession: C43016
A:Molecule type: DNA
A:Residues: 1-183 <SAN>
A:Cross-references: GB:U02459; GB:M17233; GB:M24325; GB:V00636; GB:X00906;
NID:9215104
R:Neichen, K.; Shepherd, J.C.W.; Bickley, T.A.
Nucleic Acids Res. 9, 4639-4653, 1981
A>Title: The DNA sequence of the phage lambda genome between P-L and the gene
bet.
A:Reference number: A93737; MUID:82059489; PMID:6458018
A:Accession: H93737
A:Molecule type: DNA
A:Residues: 1-183 <INE>
A:Cross-references: GB:V00638; NID:915060
A>Note: There is no known gene that maps in this region. As this region is not
overlapped by any other genes and it contains a large open reading frame, the
authors suggest that it represents a previously unidentified gene, which they
named gnt; the propose that, in conjunction with the Eal0 protein, the gnt gene
product is involved in production of the Tro phenotype
A>Note: this phenotype is expressed when phages that possess a mutant cro gene
and a thermolabile CI repressor gene are unable to propagate at restrictive

```

temperatures; this inability is correlated with the shutoff of host

macromolecular synthesis

A>Note: the authors chose Met-5 as the initial residue because it is preceded by a Shine-Dalgarno sequence

C:Genetics:

A:Gene: git

A:Map position: 71.10-72.23

C:Superfamily: phage lambda git protein

C:Keywords: transmembrane protein

QORECL Length: 183 July 16, 2003 13:37 Type: P Check: 89 ..
Found using 'var1' (kam816.key)

29 IHWGLLLSPDNWPEYVERIGIPHWVHFVFAFAESLAIVHRLSATASARYKFKLRK |-----|
79 85

89 RIKMNDKRVSVIONLTFEQSWLCAALNEGRKVVVTSKQFPYISEL

1 match found in sequence:
t38636 / TOIG of: t38636 check: 1067 from: 1 to: 1190
(from "var1pir.pep")
TOIG of: t38636 check: 1067 from: 1 to: 1190

P1;t38636 - tat binding homolog - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38636
R:McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21722
A:Accession: T38636
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1190 <MC1>
A:Cross-references: EMBL:Z98979; PIDN:CAB11703.1; GSPDB:GN00066;
SPDB:SPAC31G5.19
A:Experimental source: strain 972h-; cosmid c31G5
C:Genetics:
A:Gene: SPDB:SPAC31G5.19
A:Map position: 1

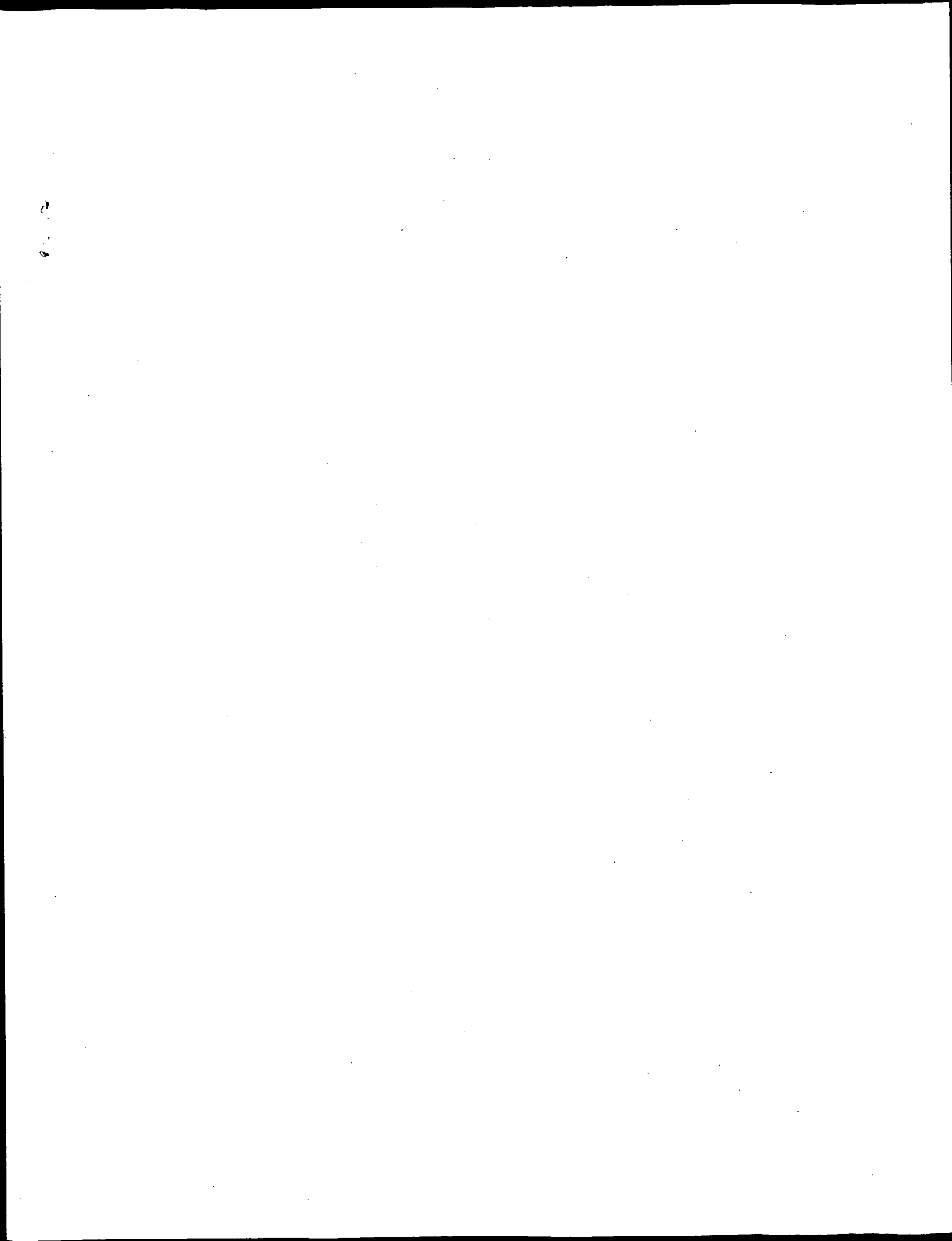
T38636 Length: 1190 July 16, 2003 13:37 Type: P Check: 1067 ..
Found using 'var1' (kam816.key)

762 KRRVLPPLAPPPPTTSOKITLKTKQADMRLNKLKIKLINALGSLRARRKFKKPL |-----|
812 818

822 IDENDIYCVDPETGHSYRSRECHYEFVDVVKQIGSDQKFSMSLE

-- Search Statistics --

| | | |
|--------------------------------|-------------|---------------|
| Times: | CPU | Total Elapsed |
| | 00:00:00.00 | 00:00:00.00 |
| Number of sequences searched: | 7 | |
| Number of sequence hits: | 7 | |
| Number of separate matches: | 7 | |
| Number of sequence hits saved: | 0 | |



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> 0 <

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Release 5.4

-- Outline of search "varl_sp" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.

Selected sequence key from "kam816.key":

varl (AA) ID: varl AA preliminary pattern

1 followed by
2 a or k or g
2 l or r
2 y
2 k or r or h
2 k or r or h
2 f
2 k or r or h

Selected files:

File : varlsp.pep

-- Output Parameters --

| Format Options: | File Options: | |
|-----------------------------|---------------|-----|
| Nucleic acid code matching | Exact | NO |
| Find non-matching hits only | No | NO |
| Report key used | Yes | Yes |
| Note position of hit | Yes | Yes |
| Display full annotations | Yes | Yes |
| Sequence context | 50 | Yes |

-- Run Parameters --

| Run mode | Batch |
|--------------------------|-------|
| Time to start comparison | now |
| Notify at end of run | NO |

1 match found in sequence:

calbnaegr ; Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)
(from "varlsp.pep")

TOIG of: calb_naegr check: 936 from: 1 to: 177

| ID | CALB_NAEGR | STANDARD: | PRT: | 177 AA. |
|----|---|-----------|------|---------|
| AC | P42322; | | | |
| DT | 01-NOV-1995 (Rel. 32, Created) | | | |
| DT | 01-NOV-1995 (Rel. 32, Last sequence update) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update) | | | |
| DE | Calcineurin B subunit (Protein phosphatase 2B regulatory subunit) | | | |
| DE | (Calcineurin regulatory subunit). | | | |
| GN | CMB1. | | | |
| OS | Naegleria gruberi. | | | |
| OS | Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria. | | | |
| OX | NCBI_TaxID=5762; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=NEG; | | | |
| RX | MEDLINE=95172399; PubMed=7867946; | | | |
| RA | Remillard S.P., Lai E.Y., Levy Y.Y., Fulton C.; | | | |
| RT | "A calcineurin-B-encoding gene expressed during differentiation of the amoeboid flagellate Naegleria gruberi contains two introns."; | | | |
| RL | Gene 154:39-45(1995). | | | |
| CC | - FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM SENSITIVITY (BY SIMILARITY). | | | |
| CC | - SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY SUBUNIT (B) (BY SIMILARITY). | | | |

CC - MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING SITES (BY SIMILARITY).
CC - SIMILARITY: Contains 4 EF-hand calcium-binding domains.
CC -----
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CC -----
CC EMBL: U04380; AAA81896.1; -.
CC HSSP: P06705; IATU.
CC InterPro: IPR002048; EF-hand.
CC InterPro: IPR001125; Recoverin.
CC Pfam: PF00036; ehand; 4.
CC PRINTS: PR00450; RECOVERIN.
CC ProDom: PD000012; EF-hand; 2.
CC SMART: SM00054; EFh; 4.
CC PROSITE: PS00018; EF_HAND; 4.
CC Calcium-binding; Repeat.
CC CA_BIND 38 49 EF-HAND 1 (BY SIMILARITY).
CC CA_BIND 70 81 EF-HAND 2 (BY SIMILARITY).
CC CA_BIND 107 118 EF-HAND 3 (BY SIMILARITY).
CC CA_BIND 148 159 EF-HAND 4 (BY SIMILARITY).
CC SEQUENCE 177 AA; 20057 MW; 01D4A48E947E97C CRC64;

CALB_NAEGR Length: 177 July 16, 2003 13:39 Type: P Check: 936
Found using 'varl' (kam816.key)

1 MGTNTSLRPEEVEEMQKGTNFTQKEIKKLYKFKKLDKDGNTISKDEPLMPELAYNP
29 35

61 LTKRVISIPDENGDSVNFKEPIAA

1 match found in sequence:

rh3aque ; Ribonuclease HIII (EC 3.1.26.-) (RNase HIII).
(from "varlsp.pep")

TOIG of: rh3_aque check: 9383 from: 1 to: 257

| ID | RNH3_AQUAE | STANDARD: | PRT: | 257 AA. |
|----|--|-----------|------|---------|
| AC | O67644; | | | |
| DT | 30-MAY-2000 (Rel. 39, Created) | | | |
| DT | 30-MAY-2000 (Rel. 39, Last sequence update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Ribonuclease HIII (EC 3.1.26.-) (RNase HIII). | | | |
| GN | RNHC OR AQ_1768. | | | |
| OS | Aquifex aeolicus. | | | |
| OS | Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex. | | | |
| OX | NCBI_TaxID=63363; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=VF5; | | | |
| RX | MEDLINE=98196666; PubMed=9537320; | | | |
| RA | Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., | | | |
| RA | Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjey M., Huber R., | | | |
| RA | Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; | | | |
| RT | "The complete genome of the hyperthermophilic bacterium Aquifex | | | |
| RL | Nature 392:353-358(1998). | | | |
| CC | - FUNCTION: This enzyme is an endonuclease that degrades the RNA of | | | |
| CC | RNA-DNA hybrids specifically (BY similarity). | | | |
| CC | - CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'- | | | |
| CC | phosphomonoester. | | | |
| CC | - COFACTOR: MAGNESIUM (BY SIMILARITY). | | | |
| CC | - SUBCELLULAR LOCATION: Cytoplasmic (potential). | | | |
| CC | - SIMILARITY: Belongs to the RNase HII family. Rhnc subfamily. | | | |

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 CC -----
 DR EMBL: AE000755; AAC07614.1; -
 DR PIR: B70452; B70452.
 DR HAMAP: MF_00053; -; 1.
 DR InterPro: IPR001352; RNase_HII/HIII.
 DR InterPro: IPR004641; RNHIII.
 DR Pfam: PF01351; RNase_HII; 1.
 DR TIGRFAMs: TIGR00716; rnhC; 1.
 KW Hydrolase; Nuclease; Endonuclease; Magnesium; Complete proteome.
 FT ACT_SITE 77 77 BY SIMILARITY.
 FT ACT_SITE 179 179 BY SIMILARITY.
 SQ SEQUENCE 257 AA; 29538 MW; 184FC7B5431F9607 CRC64;
 RNH3_AQUAE Length: 257 July 16, 2003 13:39 Type: P Check: 9383
 Found using 'varl' (kam816.key)

94 CIPENNYLVSSLNPRDTRKLSDKREERLYLALPKLVKACYEIKPEYNYLKRFRNLN
 144 150

154 KMTTFYKLLIERVKEGSGSEVVVDKYPNSPFGEDVIFTEAERN

1 match found in sequence:
 stieb_lambd : Superinfection exclusion protein B.
 (from "varisp.pep")
 TOIG of: stieb_lambd check: 89 from: 1 to: 183

ID SIEB_LAMB STANDARD: PRT; 183 AA.
 AC P03762;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Superinfection exclusion protein B.
 GN SIEB OR GIT.
 OS Bacteriophage lambda.
 CC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 CC Lambda-like viruses.
 CC NCBI_TaxID=10710;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83189071; PubMed=6221115;
 RA Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.;
 RT "Nucleotide sequence of bacteriophage lambda DNA.";
 RL J. Mol. Biol. 162:729-773(1982).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82059489; PubMed=6458018;
 RA Inelichen K., Shepherd J.C.W., Bickle T.A.;
 RT "The DNA sequence of the phage lambda genome between PL and the gene
 bet.";
 RL Nucleic Acids Res. 9:4639-4653(1981).
 RN [3]
 RP IDENTIFICATION.
 RX MEDLINE=93328675; PubMed=8335629;
 RA Ranade K., Potete A.R.;
 RT "Superinfection exclusion (sieb) genes of bacteriophages P22 and
 lambda.";
 RL J. Bacteriol. 175:4712-4718(1993).
 CC -1- FUNCTION: HAS A ROLE IN THE PREVENTION OF SUPERINFECTION BY
 CC PHAGES THAT ARE INSENSITIVE TO REPRESSION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
 CC -----
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 CC -----
 DR EMBL: J02459; -; NOT_ANNOTATED_CDS.
 DR EMBL: Y00638; CAA23982.1; ALT_INIT.
 DR PIR: I43010; QOBPGU.
 DR Transmembrane.
 KW TRANSMEM 22 38 POTENTIAL.
 FT TRANSMEM 54 70 POTENTIAL.
 SQ SEQUENCE 183 AA; 21426 MW; F9D1F9CAD886A9A CRC64;
 SIEB_LAMB Length: 183 July 16, 2003 13:39 Type: P Check: 89
 Found using 'varl' (kam816.key)

29 IWGGLISPDNMPDYNERIGIPHWVHFVFAFAFSLAINVHRLSAISARKRKLRK
 79 85

89 RIKQNDKRVSTIONLTEQSNVLCALNEGKRYVTSKOPYISEL

1 match found in sequence:
 yel9oceih : Hypothetical protein OB1419.
 (from "varisp.pep")
 TOIG of: yel9_ocien check: 4790 from: 1 to: 88

ID YEL9_OCEIH STANDARD: PRT; 88 AA.
 AC P59153;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein OB1419.
 GN OB1419.
 OS Oceanobacillus iheyensis.
 CC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Oceanobacillus.
 CC NCBI_TaxID=182710;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
 RX MEDLINE=2220767; PubMed=12235376;
 RA Takami H., Takaki Y., Uchiyama I.;
 RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
 RT Ridge and its unexpected adaptive capabilities to extreme
 RT environments.";
 RL Nucleic Acids Res. 30:3927-3935(2002).
 RN [2]
 RP -1- SIMILARITY: BELONGS TO THE UPF0223 FAMILY.
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 CC -----
 DR EMBL: AP004597; BAC13375.1; -
 DR HAMAP: MF_01041; -; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 88 AA; 10584 MW; C27D1A2A0CP3517A CRC64;
 YEL9_OCEIH Length: 88 July 16, 2003 13:39 Type: P Check: 4790
 Found using 'varl' (kam816.key)

1 MSYQPMDETMTSTEDIDVNFSLIEKAYEKQVDREILALYRFKQIVSKSEKKLF
41 47

Number of sequences searched: 5
Number of sequence hits: 5
Number of separate matches: 5
Number of sequence hits saved: 0

61 TQDEASGYSYHVYKARETNESNIRM

1 match found in sequence:

Y926metja; Hypothetical protein MJ1626.
(from "var1sp.pep")

TOIG of: Y926_metja check: 5094 from: 1 to: 765

ID Y926_METJA STANDARD: PRT: 765 AA.
AC O59019;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein MJ1626.
GN MJ1626.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JA-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337993; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Uutterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
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CC -----
CC EMBL: U67602; AAB99649.1; -
DR PIR: G64502; G64502.
DR TIGR: MJ1626; -
KW Hypothetical protein; Complete proteome.
SO SEQUENCE 765 AA; 89606 MW; 056EAA4FEF9B098 CRC64;

Y926_METJA Length: 765 July 16, 2003 13:39 Type: P Check: 5094
Found using 'var1' (kam816.key)

230 ILANKLYSSEKDERELTNILNIVDSLTDEQKNILRGHLVSLSLGDDEKRYRKPKOLF
280 286

290 EKLIPALSDQIKSLKSHGKTTNIIILRENIKLPANFYNNREELK

-- Search Statistics --

Times: CPU Total Elapsed
00:00:00.00 00:00:01.00

3

7

> 0 <
01/10 Intelligenetics
> 0 <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "varl_spt" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence. "kam816.key":

Selected sequence key from "kam816.key":
varl (AA) ID varl AA preliminary pattern
Followed by
1 a or k or g
2 y
2 l or r
2 k or r or h
2 k or r or h
2 f
2 k or r or h

Selected files:

File : varlspt.pep

-- Output Parameters --

Format Options: File Options:
Nucleic acid code matching Exact Indirect file
Find non-matching hits only No Sequence or key file
Report key used Yes List of hits
Note position of hit Yes Hit display
Display full annotations Yes Name and annotations
Sequence context 50

-- Run Parameters --

Run mode Batch
Time to start comparison now
Notify at end of run No

1 match found in sequence:

014114 ; Tat-binding homolog 7, AAA ATPase family protein.
(from "varlspt.pep")

TOIG of: 014114 Check: 1067 from: 1 to: 1190

ID 014114 PRELIMINARY; PRT; 1190 AA.
AC 014114;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Tat-binding homolog 7, AAA ATPase family protein.
GN SPAC31G5.19.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCB1_TaxID=4896;
[1]
RN NCB1_TaxID=4896;
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA McLean J., Harris D.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; 298979; CAB11703.1; -.
DR GenedB_Spombe; SPAC31G5.19; -.

DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_centrl.
DR InterPro; IPR003960; AAA_sub.
DR Pfam; PF00004; AAA; 1.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00674; AAA; 1.
KW ATP-binding.
SQ SEQUENCE 1190 AA; 135350 MW; 44F5FE817DB18DC CRC64;

014114 Length: 1190 July 16, 2003 13:40 Type: P Check: 1067
Found using 'varl' (kam816.key)

762 KRRVLPPLAPDPPTTSQITLTKQTKQADMLNKLKIKLNALLGSLRARRKPKPL
IDFNDIYCVDPETGHSYRSRECHYEFVDVYKQIGSDOKFSMSLSL
812 818

1 match found in sequence:

031001 ; DNA polymerase III holoenzyme tau subunit.
(from "varlspt.pep")

TOIG of: 031001 Check: 888 from: 1 to: 529

ID 031001 PRELIMINARY; PRT; 529 AA.
AC 031001;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE DNA polymerase III holoenzyme tau subunit.
GN DNAX.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCB1_TaxID=274;
[1]
RN NCB1_TaxID=274;
RP SEQUENCE FROM N.A.
RC STRAIN=PMF48.KAT;
RX MEDLINE=97446162; PubMed=9299346;
RA McHenry C.S., Seville M., Cull M.G.;
RT "A DNA polymerase III holoenzyme-like subassembly from an extreme
thermophilic eubacterium."
RL J. Mol. Biol. 272:178-189(1997).
DR EMBL; AF025391; AAB82595.1; -.
DR HSSP; P28631; 1A5T.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_centrl.
DR InterPro; IPR001270; Chaprinin_C1PA/B.
DR InterPro; IPR000862; Rfcdomain.
DR Pfam; PF00004; AAA; 1.
DR PRINTS; PR00300; CLPPTREASPA.
DR SMART; SM00382; AAA; 1.
KW ATP-binding.
SQ SEQUENCE 529 AA; 58162 MW; 0852FA62DFFEE33 CRC64;

031001 Length: 529 July 16, 2003 13:40 Type: P Check: 888
Found using 'varl' (kam816.key)

1 MSALYRFRPPLTFQEVNGEHNKPEPLKAIKRGRLAQAAYLFSGPRGVKTTTARLAMA
3 9

1 match found in sequence:

055649 ; Pg-1.

(from "varlspt.pep")

TOIG of: 055649 Check: 519 from: 1 to: 347

ID 055649 PRELIMINARY; PRT; 347 AA.
 AC 055649;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE p9-1.
 OS Rice black streaked dwarf virus (RBSV).
 OC Viruses; dsRNA viruses; Reoviridae; Filivirus.
 NCBI_TaxID=10990;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98295849; PubMed=9634092;
 RA Isogai M., Uyeda I., Lee B.-C.;
 RT "Detection and assignment of proteins encoded by rice black streaked
 dwarf filivirus S7, S8, S9, and S10.";
 RL J. Gen. Virol. 79:1487-1494(1998).
 DR EMBL: AB014403; BAA25081.1;
 SQ SEQUENCE 347 AA; 39877 MW; BODEB7C6A0E7B66 CRC64;

055649 Length: 347 July 16, 2003 13:40 Type: P Check: 519
 Found using 'varl' (kam816.key)

269 SLISTPALIREKIAEGLEFRIITSNALNGAPROTVLFRINGSESEFLNKRYKRRFRREY
 319 325
 329 AGNDVSVIKSPFSLKIDV

1 match found in sequence:
 057768 : Hypothetical protein PH0012.
 (from "varispt.pep")
 TOIG of: 057768 check: 5893 from: 1 to: 269

ID 057768 PRELIMINARY; PRT; 269 AA.
 AC 057768;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein PH0012.
 GN PH0012.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 NCBI_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Hatakeyama Y., Hino Y.,
 Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohnuki Y.,
 Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
 Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 DR EMBL: AP000001; BAA29080.1;
 DR InterPro: IPR000182; GCS5aceyl1transf.
 DR Pfam: PF00583; Acetyl1transf.1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 269 AA; 30843 MW; 67B352B36B6770A CRC64;

057768 Length: 269 July 16, 2003 13:40 Type: P Check: 5893
 Found using 'varl' (kam816.key)

63 FYNQAWIGIMGVKKAAYORRGIGTEVFRRLEIGRRKVDITRLDASSGYLYKKFKFVD
 113 119

123 EYTVRYELMERPIKRVESVEVNKIPMWKEIDKAFGDRIAYLE

1 match found in sequence:
 084486 : Oligopeptide binding lipoprotein.
 (from "varispt.pep")
 TOIG of: 084486 check: 2099 from: 1 to: 696

ID 084486 PRELIMINARY; PRT; 696 AA.
 AC 084486;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Oligopeptide binding lipoprotein.
 GN OPPA_4 OR CT480.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D/DW-3/CX;
 RX MEDLINE=99000809; PubMed=9784136;
 RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
 Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans:
 Chlamydia trachomatis.";
 RL Science 282:754-759(1998).
 DR EMBL: AE001321; AAC68080.1;
 DR InterPro: IPR000914; SBP_bac-5.
 DR Pfam: PF00496; SBP_bac-5; 1.
 KW Lipoprotein; Complete proteome.
 SQ SEQUENCE 696 AA; 79890 MW; 8531E6CB1D80079 CRC64;

084486 Length: 696 July 16, 2003 13:40 Type: P Check: 2099
 Found using 'varl' (kam816.key)

576 LGTPEDPALMHSEGALEKGSANAVGFCNEADRIIEQLSYEDSNKROALYHRRFHEV
 626 632

636 HESPYAFIYSROYSLVYKEFVNINIPVTPHODLLPGADETVNLNM

1 match found in sequence:
 98bc69 : Hypothetical protein.
 (from "varispt.pep")

TOIG of: 98bc69 check: 1570 from: 1 to: 347

ID 08bc69 PRELIMINARY; PRT; 347 AA.
 AC 08bc69;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Rice black streaked dwarf virus (RBSV).
 OC Viruses; dsRNA viruses; Reoviridae; Filivirus.
 NCBI_TaxID=10990;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Henan Zhengzhou;
 RA Li C., Zhong Y.;
 RT "Cloning and Expression of s9-1 gene of Rice Black-Streaked Dwarf
 virus in Escherichia coli.";

RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF540976; AAN28667.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 347 AA; 39854 MW; 6509703242121D48 CRC64;
 Found using 'varl' (Kam816.key)

269 SLSITPALIREKIAKEGLFKITITSNLRGASROTVLFRGNGSESEFLNKRKRPRTRI
 319 325
 329 VGNVDCVIRKSPFSSLKLDV

1 match found in sequence:
 q8155 ; Hypothetical protein.
 (from "varispt.pep")
 TOIG of: q8155 check: 1074 from: 1 to: 1352

ID O81155 PRELIMINARY; PRT; 1352 AA.
 AC O81155;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE Hypothetical protein.
 GN PF11_0319.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3D7;
 RX MEDLINE=22255705; Pubmed=12368864;
 RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
 RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
 RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angiuoli S.,
 RA Perlea M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
 RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings I.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.;
 RT "Genome sequence of the human malaria parasite Plasmodium
 falciparum";
 RL Nature 419:498-511(2002).
 DR EMBL: AE014840; AAN35903.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 1352 AA; 165114 MW; 85FC8349EFAA8946 CRC64;
 O81155 Length: 1352 July 16, 2003 13:40 Type: P Check: 1074
 Found using 'varl' (Kam816.key)

797 VIMSFTYLSFLKCYNTTYSRLINLILRVNKEVCIKHLPYVIGIMNFFKLYKKFKILK
 847 853
 857 YKEKEEYKDYDENLNKNDLYEQDNISMFNDRYYNKELEKTKIKRKEK

1 match found in sequence:
 q812v6 ; Evolutionarily conserved G-patch domain containing protein.
 (from "varispt.pep")
 TOIG of: q812v6 check: 1296 from: 1 to: 931
 ID O812V6 PRELIMINARY; PRT; 931 AA.
 AC O812V6;

DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Evolutionarily conserved G-patch domain containing protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bladder;
 RA Luallen R.J., Sargeant R., Geng Y.,
 RT "Cloning of an Evolutionarily Conserved G-patch Domain Containing
 RT Protein";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF434677; AAN63596.1; -
 SQ SEQUENCE 931 AA; 103285 MW; 9271E1DFA64906F5 CRC64;
 O812V6 Length: 931 July 16, 2003 13:40 Type: P Check: 1296
 Found using 'varl' (Kam816.key)

1 MAARDSEEDLVSYGTGLFPLEGERPKRPIPLQDQTVRDEKGRYKRFHGAFFSGGSAG
 44 50
 61 YFNVTGSKEGWPTFTVSSRONRADKSVLGPEDFMEEDL

1 match found in sequence:
 q8kx8 ; Sex pilus assembly.
 (from "varispt.pep")
 TOIG of: q8kx8 check: 3730 from: 1 to: 95

ID O8K0X8 PRELIMINARY; PRT; 95 AA.
 AC O8K0X8;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DE Sex pilus assembly.
 GN TRAL.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22103115; Pubmed=12107144;
 RA Beaber J.W., Hochhut B., Waldor M.K.,
 RT "Genomic and Functional Analyses of SXT, an Integrating Antibiotic
 RT Resistance Gene Transfer Element Derived from Vibrio cholerae";
 RL J. Bacteriol. 184:4259-4269(2002).
 DR EMBL: AY05428; AAL59674.1; -
 SQ SEQUENCE 95 AA; 10669 MW; 098A0BDD6AC5EC0C CRC64;
 O8K0X8 Length: 95 July 16, 2003 13:40 Type: P Check: 3730
 Found using 'varl' (Kam816.key)

4 EPVNIPSYIDDPHPFLMSADEKAPILGLVIGFTGNALVYLGLVTTKIKYRFRGR
 54 60

64 PDGFIHAITYWAGLPTKAKTIPNPPIRSYLP
 1 match found in sequence:
 q81x11 ; Ribosomal protein S4.
 (from "varispt.pep")
 TOIG of: q81x11 check: 7065 from: 1 to: 265

ID OBLX11 PRELIMINARY; PRT; 265 AA.
 AC OBLX11;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
 DE Ribosomal protein S4.
 GN RPS4.
 OS Laminaria digitata.
 OG Mitochondrion.
 OC Eukaryota; Stramenopiles; Phaeophyceae; Laminariales; Laminariaceae;
 CC Laminaria;
 OX NCBI_TaxID=80365;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Oudet-le secq M.-P., Kloareg B., Loiseaux-de-Goer S.;
 RT "The mitochondrial genome of the brown alga Laminaria digitata: a
 comparative analysis.";
 RL Eur. J. Phycol. 37:163-172(2002).
 DR EMBL; AJ344328; CAC87949.1; -
 DR InterPro: IPR002942; S4.
 DR Pfam: PF01479; S4; 1.
 DR SMART: SM00363; S4; 1.
 KW Mitochondrion.
 SQ SEQUENCE 265 AA; 31709 MW; 02727BCD1A3E6A7A CRC64;
 OBLX11 Length: 265 July 16, 2003 13:40 Type: P Check: 7065
 Found using 'varl' (kam816.key)

142 HSIYRSRSTFHNKVIYNGKKIGHGFILOKGDYVERCPSQSRATRAVLARFKRRSSH
 192 198
 202 VKLERWRLSNRKFELHPTPKWVGDTYNSLFTSSDYCAPVMT

1 match found in sequence:
 g8mgt6; Protein phosphatase 2B regulatory subunit.
 (from "varlspt.pep")
 TOIG of: g8mgt6 check: 2094 from: 1 to: 177

ID O8MGT6 PRELIMINARY; PRT; 177 AA.
 AC O8MGT6;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
 DE Protein phosphatase 2B regulatory subunit.
 GN CNB.
 OS Toxoplasma gondii.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida; Sarcocystidae;
 CC Toxoplasma.
 OX NCBI_TaxID=5811;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gaskins E., Kleschick H., Beckers C.J.;
 RT "Identification of the calcineurin A and B subunits of Toxoplasma
 gondii.";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY125926; AAM97279.1; -
 DR InterPro: IPR003299; Calflagin.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001125; Recoverin.
 DR Pfam: PF00036; ehand; 4.
 DR PRINTS: PRO1362; CALFLAGIN.
 DR PRINTS: PRO0450; RECOVERIN.
 DR ProDom: PD000012; EF-hand; 2.
 DR PROSITE: PS00018; EF-hand; 4.
 SO SEQUENCE 177 AA; 19994 MW; D5888EC014F569D8 CRC64;

O8MGT6 Length: 177 July 16, 2003 13:40 Type: P Check: 2094

Found using 'varl' (kam816.key)

1 MGNAGRLSPQEQMDILHANFSEKDLKLYKRFALPTNONGELDTHELFDVPELADNP
 29 35

61 LVKRVLSIFDTNGDKVSVFEFLVG

1 match found in sequence:
 g8n3b7; Hypothetical protein (Fragment).
 (from "varlspt.pep")
 TOIG of: g8n3b7 check: 3543 from: 1 to: 932

ID O8N3B7 PRELIMINARY; PRT; 932 AA.
 AC O8N3B7;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
 DE Hypothetical protein (Fragment).
 GN DKFZP76211110.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Melanoma.
 RA Blum H., Bauersachs S., Mewes H.W., Weil B., Wiemann S.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL834465; CAD39124.1; -
 DR InterPro: IPR000467; G_patch.
 DR Pfam: PF01585; G_patch; 1.
 DR PROSITE: PSS0174; G_PATCH; 1.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 932 AA; 103518 MW; CA3724C297FD250D CRC64;

O8N3B7 Length: 932 July 16, 2003 13:40 Type: P Check: 3543
 Found using 'varl' (kam816.key)

1 DAMAFDSSEEDLVSYGTGLEPLEGERPKKPIPLDQYVRDEKGYKRFHAFSGGFA
 43 51

61 GYFNTVGSKEGWTPTSTVSSRQNRADKSVLGPEDFMEDEDL

1 match found in sequence:
 g8pa45; Hypothetical protein XCC1648.
 (from "varlspt.pep")
 TOIG of: g8pa45 check: 6700 from: 1 to: 78

ID O8PA45 PRELIMINARY; PRT; 78 AA.
 AC O8PA45;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, last annotation update)
 DE Hypothetical protein XCC1648.
 GN XCC1648.
 OS Xanthomonas campestris (pv. campestris).
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 CC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33913 / NCPPB 528;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

329 VGNVDCV IKSDFSS LKLDV

1 match found in sequence:
g913e4 : Hypothetical 39.9 kDa protein.

(from "varispt.pep")
TOIG of: g913e4 check: 1822 from: 1 to: 347

ID G913E4 PRELIMINARY; PRT; 347 AA.
AC G913E4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical 39.9 kDa protein.
OS Rice black streaked dwarf virus (RBSDV).
OC Viruses; dsRNA viruses; Reoviridae; Filiviruses.
OX NCBI_TaxID=10990;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=zhjw;
RA Bai F., Qu Z., Xu J., Ye M., Shen D.;
RT "Rice black streaked dwarf virus segment 9 isolate zhjw.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=zhjs;
RA Bai F., Qu Z., Yan J., Xu J., Shen D.;
RT "Rice black streaked dwarf virus segment 9 isolate zhjs.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY050486; AAL13111.1; -;
DR EMBL: AF459812; AAL6344.1; -;
KW Hypothetical protein 39942 MW; BF5680E237489E34 CRC64;
SQ SEQUENCE 347 AA; 39942 MW; BF5680E237489E34 CRC64;

G913e4 Length: 347 July 16, 2003 13:40 Type: P Check: 1822
Found using 'varl' (kam816.key)

269 SSLISTPALIREKIAEGLEFKITTSNTLRGASROTIVLFRGINGSSEFLNIKKRRKRRRI
319 325

329 VGNVDCVIKSDPSSIKLDV

1 match found in sequence:
g91e13 : Hypothetical protein (40 kDa protein).

(from "varispt.pep")
TOIG of: g91e13 check: 525 from: 1 to: 347

ID G91E13 PRELIMINARY; PRT; 347 AA.
AC G91E13;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Hypothetical protein (40 kDa protein).
OS Rice black streaked dwarf virus (RBSDV).
OC Viruses; dsRNA viruses; Reoviridae; Filiviruses.
OX NCBI_TaxID=10990;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang H., Chen J., Lei J., Adams M.J.;
RT "Sequence analysis shows that a dwarfing disease on rice, wheat and
maize in China is caused by Rice black-streaked dwarf virus (RBSDV).";
RL Eur. J. Plant Pathol. 107:563-567(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Sun L., Fang S., Yu J.;
RT "Nucleotide sequence of rice black-streaked dwarf virus fragment 9.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ297420; CAC59968.1; -;
DR EMBL: AF536564; AAN04489.1; -;
KW Hypothetical protein.
SQ SEQUENCE 347 AA; 39962 MW; 2979A7F62266917 CRC64;

G91E13 Length: 347 July 16, 2003 13:40 Type: P Check: 525
Found using 'varl' (kam816.key)

269 SSLISTPALIREKIAEGLEFKITTSNTLRGASROTIVLFRGINGSSEFLNIKKRRKRRRI
319 325

329 VGNVDCVIKSDPSSIKLDV

1 match found in sequence:
g91e14 : Hypothetical 40.0 kDa protein.

(from "varispt.pep")
TOIG of: g91e14 check: 9914 from: 1 to: 347

ID G91E14 PRELIMINARY; PRT; 347 AA.
AC G91E14;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 40.0 kDa protein.
OS Rice black streaked dwarf virus (RBSDV).
OC Viruses; dsRNA viruses; Reoviridae; Filiviruses.
OX NCBI_TaxID=10990;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang H., Chen J., Lei J., Adams M.J.;
RT "Sequence analysis shows that a dwarfing disease on rice, wheat and
maize in China is caused by Rice black-streaked dwarf virus (RBSDV).";
RL Eur. J. Plant Pathol. 107:563-567(2001).
DR EMBL: AJ297420; CAC59968.1; -;
KW Hypothetical protein.
SQ SEQUENCE 347 AA; 39968 MW; E799BCB488A37B72 CRC64;

G91E14 Length: 347 July 16, 2003 13:40 Type: P Check: 9914
Found using 'varl' (kam816.key)

269 SSLISTPALIREKIAEGLEFKITTSNTLRGASROTIVLFRGINGSSEFLNIKKRRKRRRI
319 325

329 VGNVDCVIKSDPSSIKLDV

1 match found in sequence:
g91e20 : P9-1 protein.

(from "varispt.pep")
TOIG of: g91e20 check: 754 from: 1 to: 347

ID G91E20 PRELIMINARY; PRT; 347 AA.
AC G91E20;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE P9-1 protein.
OS Rice black streaked dwarf virus (RBSDV).
OC Viruses; dsRNA viruses; Reoviridae; Filiviruses.
OX NCBI_TaxID=10990;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wuhan S9;
RA Zhang H., Chen J., Lei J., Adams M.J.;
RT "Sequence analysis shows that a dwarfing disease on rice, wheat and
maize in China is caused by Rice black-streaked dwarf virus (RBSDV).";
RL Eur. J. Plant Pathol. 107:563-567(2001).
DR EMBL: AJ291706; CAC59959.1; -;
KW Hypothetical protein.
SQ SEQUENCE 347 AA; 39896 MW; B33A4BF0EDD98614 CRC64;

091H02 Length: 347 July 16, 2003 13:40 Type: P Check: 754 ..
Found using 'varl' (kam816.key)

269 SSLISTPALIREKIAKGLFKITISNTLRGASROTVLFRGINGSSEFLNKRKRPRTI
VGNDVCVAKSDPSSLKLDV 319 325

1 match found in sequence:
q91h02 ; Hypothetical 39.9 kDa protein.
(from "varlspt.pep")
TOIG of: q91h02 check: 183 from: 1 to: 347

ID Q91H02 PRELIMINARY; PRT; 347 AA.
AC Q91H02;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Hypothetical 39.9 kDa protein.
OS Rice black streaked dwarf virus (RBSDV).
OC Viruses; dsRNA viruses; Reoviridae; Filiviruses.
OX NCBI_TaxID=10990;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-Shandong;
RA Bai F., Qu Z., Xu J., Ye M., Shen D.;
RT "Rice black streaked dwarf virus genome segment 9."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY039705; AAK73172.1;
KW Hypothetical protein.
SQ SEQUENCE 347 AA; 39897 MW; 6FB9EF7D7C63421B CRC64;

Q91H02 Length: 347 July 16, 2003 13:40 Type: P Check: 183 ..
Found using 'varl' (kam816.key)

269 SSLISTPALIREKIAKGLFKITISNTLRGASROTVLFRGINGSSEFLNKRKRPRTI
VGNDVCVAKSDPSSLKLDV 319 325

1 match found in sequence:
q94z19 ; Ribosomal protein S4.
(from "varlspt.pep")
TOIG of: q94z19 check: 8109 from: 1 to: 265

ID Q94Z19 PRELIMINARY; PRT; 265 AA.
AC Q94Z19;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Ribosomal protein S4.
GN RPS4.
OS Pytaelia littoralis.
OC Mitochondrion.
OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;
OC Acinetosporaceae; Pytaelia.
OX NCBI_TaxID=2885;
RN [1]
RP SEQUENCE FROM N.A.
RA Oudot M.P.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21372210; PubMed=11479679;
RA Oudot M.P., Fontaine J.M., Rousvoal S., Kioareg B.,

RA Loiseaux-de Goer S.;
RT "The complete sequence of a brown algal mitochondrial genome, the
RT Ectocarpale Pytaelia littoralis (L.) Kjellm.";
RL J. Mol. Evol. 53:80-88(2001).
DR EMBL: AJ277126; CAC50825.1; ..
DR InterPro: IPR002942; S4.
DR Pfam: PF01479; S4; 1.
DR SMART: SM00363; S4; 1.
KW Mitochondrion.

SQ SEQUENCE 265 AA; 31720 MW; 21EEDF701B6D12F0 CRC64;

Q94Z19 Length: 265 July 16, 2003 13:40 Type: P Check: 8109 ..
Found using 'varl' (kam816.key)

142 HSIYYSRQAIQHNKIIVNGKMGSGFVLKGDYVECPORSAIRLARIYKRRPSSD
192 198

202 VRSVVRRLAHRYKLGQLQPTPKWIOTDYSLSFLSSICPPFWMP

1 match found in sequence:
q971r9 ; Glutathione peroxidase.
(from "varlspt.pep")
TOIG of: q971r9 check: 8978 from: 1 to: 181

ID Q971R9 PRELIMINARY; PRT; 181 AA.
AC Q971R9;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE Glutathione peroxidase.
GN CAC1571.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hill J., Wolf Y.I.,
RA Tatusov R.L., Sabath F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007667; AAK79538.1; ..
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam: PF00255; GSHpx; 1.
DR PRINTS: PR01011; GLUTPROXDAE.
DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
KW Peroxidase; Complete proteome.
SQ SEQUENCE 181 AA; 20870 MW; D688BDDC0C27D49C CRC64;

Q971R9 Length: 181 July 16, 2003 13:40 Type: P Check: 8978 ..
Found using 'varl' (kam816.key)

1 MSITDFKVDKINGEDISMEYRGKALLIVNTASKGFTPDYEDLALYKRGGENFEVLG
46 52
61 FPCNGFENQEPGTNNDIKKFCQINGVTFKIPDKVDVNGENE

1 match found in sequence:
 gbrr8 : Similar to RIKEN cDNA 1300003A17 gene.
 (from "var1spt.pep")
 TOIG of: gbrr8 check: 1310 from: 1 to: 931

ID Q9BRR8 PRELIMINARY; PRT; 931 AA.
 AC Q9BRR8;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Similar to RIKEN cDNA 1300003A17 gene.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC006108; AA06108.1; -
 DR InterPro: IPR000467; G_patch.
 DR Pfam: PF01585; G_patch; 1.
 DR SMART: SM00443; G_patch; 1.
 DR PROSITE: PS50174; G_PATCH; 1.
 SQ SEQUENCE 931 AA; 103345 MW; 407082BEC44904F4 CRC64;

Q9BRR8 Length: 931 July 16, 2003 13:40 Type: P Check: 1310 ..
 Found using 'var1' (kam816.key)

1 MAALSDSEEDLISYGTGLEPLEGEGRRPKPIPLDQTVRDEKGRYKRFHGAFFSGGFSAG
 44 50
 61 YFNTVSGKEGWTPTFVSSRQNRADKSLVGPEDFDEEDL

1 match found in sequence:
 g9dbm1 : 1300003A17Rik protein.
 (from "var1spt.pep")
 TOIG of: g9dbm1 check: 1796 from: 1 to: 930

ID Q9DBM1 PRELIMINARY; PRT; 930 AA.
 AC Q9DBM1;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE 1300003A17Rik protein.
 GN 1300003A17Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathii; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochika H.,
 Kuehl P., Lewis S., Matsuo Y., Nikolaic I., Pesole G., Quackenbush J.,
 Schiemi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee K.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 DR EMBL: AK004668; BAB23629.1; -
 DR MGD: MGI:1914721; 1300003A17Rik.
 DR InterPro: IPR000467; G_patch.
 DR Pfam: PF01585; G_patch; 1.
 DR SMART: SM00443; G_patch; 1.
 DR PROSITE: PS50174; G_PATCH; 1.
 SQ SEQUENCE 930 AA; 103307 MW; 62D383B72424EF73 CRC64;

Q9DBM1 Length: 930 July 16, 2003 13:40 Type: P Check: 1796 ..
 Found using 'var1' (kam816.key)

1 MAALSDSEEDLISYGTGLEPLEGEGRRPKPIPLDQTVRDEKGRYKRFHGAFFSGGFSAG
 44 50
 61 YFNTVSGKEGWTPTFVSSRQNRADKSLVGPEDFDEEDL

1 match found in sequence:
 g9p7b3 : Calcium permease family membrane transporter.
 (from "var1spt.pep")
 TOIG of: g9p7b3 check: 6779 from: 1 to: 881

ID Q9P7B3 PRELIMINARY; PRT; 881 AA.
 AC Q9P7B3;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Calcium permease family membrane transporter.
 GN SPAC521.04C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_Taxid=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972h-;
 RA Brown S., Harris D., Wood V., Rajandream M.A., Barrell B.G.,
 RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AL163481; CAB86468.1; -
 DR GeneDB: Spombe; SPAC521.04C; -
 DR InterPro: IPR005185; DUF307.
 DR InterPro: IPR001092; HLH_basic.
 DR InterPro: IPR004837; NaCa_Exmemb.
 DR Pfam: PF03733; DUF307; 1.
 DR Pfam: PF01699; Na_Ca_Ex; 2.
 DR PROSITE: PS00038; HLH_1; 1.
 SQ SEQUENCE 881 AA; 98857 MW; 4190EBF883196C4 CRC64;

Q9P7B3 Length: 881 July 16, 2003 13:40 Type: P Check: 6779 ..
 Found using 'var1' (kam816.key)

118 IPKONFVRLSPRLRGOSPASLSSESFTLKEKQNAINKTRARGMLKMPALYKKRRSIN
 168 174
 178 RDADIDIDHDEPLKRPNTSISNVIWLCFAGAPLFLVIFICYIFFTVLS

1 match found in sequence:

q9rp72 : Hypothetical 81.0 kDa protein.
 (from "var1spt.pep")
 TOIG of: q9rp72 check: 2853 from: 1 to: 706

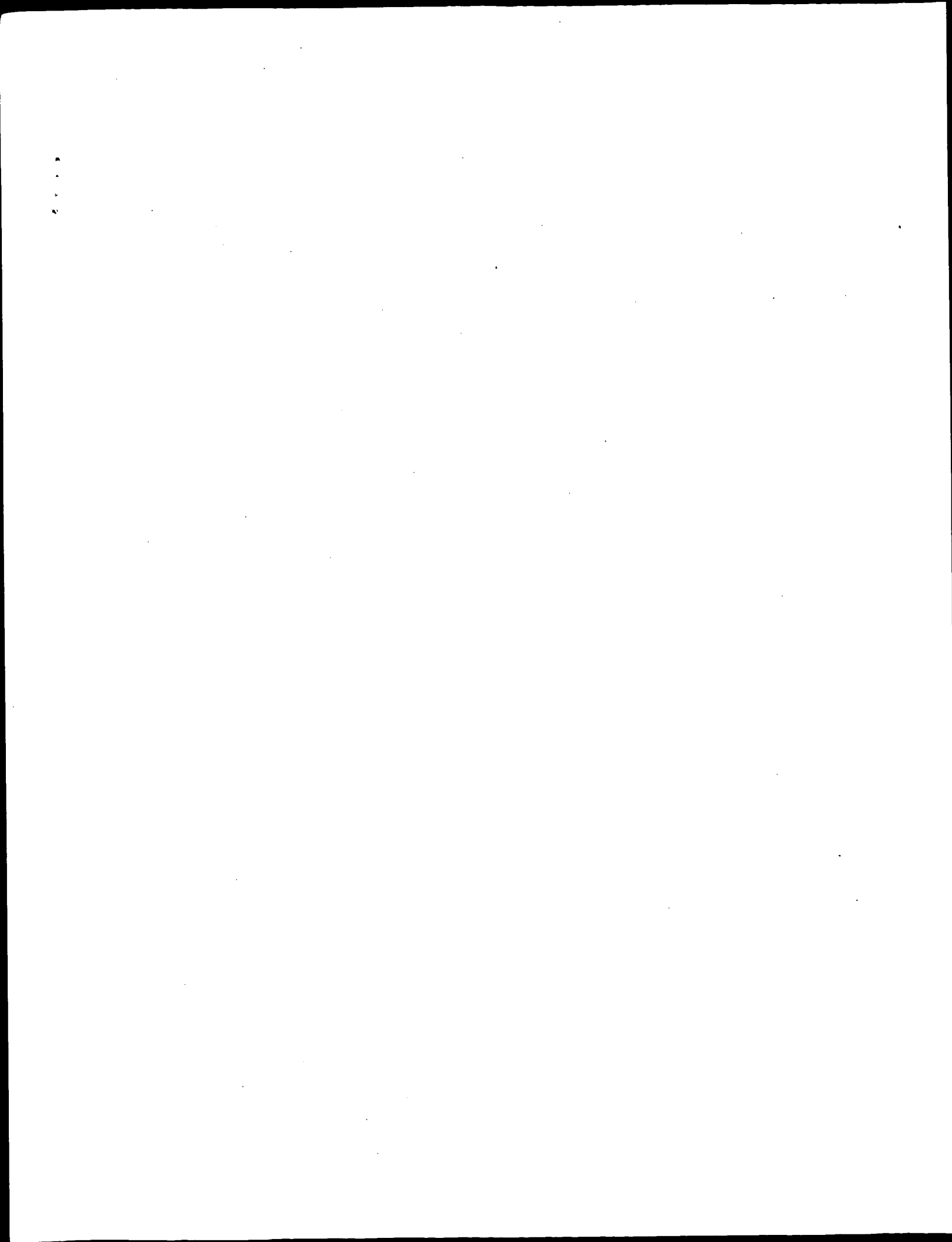
ID Q9RP72 PRELIMINARY; PRT; 706 AA.
 AC Q9RP72;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Hypothetical 81.0 kDa protein.
 OS Pasteurella haemolytica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21295097; PubMed=11401986;
 RA Lo R.Y.C., McKerral L.J., Hills T.L., Kozlowska M.;
 RT "Analysis of the Capsule Biosynthetic Locus of Mannheimia
 (Pasteurella) haemolytica A1 and Proposal of a Nomenclature System.";
 RL Infect. Immun. 69:4458-4464(2001).
 DR EMBL: AF170495; AAF08247.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 706 AA; 81021 MW; D80B20C2145F0D37 CRC64;

Q9RP72 Length: 706 July 16, 2003 13:40 Type: P Check: 2853 ..
 Found using 'var1' (kam816.key)

342 KKQMDMLPALLAYNGCIYDRASKDTSGKAYAPQYTHLIREGVNFNEIVKLYKKFVFL |-----|
 392 398
 402 NVNITOSTTMSRRVYELLASGTPVSTPSKAITAOPFGIVITVNN

-- Search Statistics --

| Times: | CPU | Total Elapsed |
|--------------------------------|-------------|---------------|
| | 00:00:00.00 | 00:00:00.00 |
| Number of sequences searched: | | 27 |
| Number of sequence hits: | | 27 |
| Number of separate matches: | | 27 |
| Number of sequence hits saved: | | 0 |



> 0 <
01 10 Intelligenetics
> 0 <
Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "var2_sp" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.

Selected sequence key from "kam816.key":

var2 (AA) ID var2 AA preliminary pattern
1 followed by
2 a or k or g
2 l or r
2 y
2 k or r or h
2 k or r or h
2 w
2

Selected files:

File : var2sp.pep

-- Output Parameters --

| Format Options: | File Options: | |
|-----------------------------|----------------------|-----|
| Nucleic acid code matching | Exact | No |
| Find non-matching hits only | Indirect file | No |
| Report key used | Sequence or key file | No |
| Note position of hit | List of hits | Yes |
| Display full annotations | Hit display | Yes |
| Sequence context | Name and annotations | Yes |

-- Run Parameters --

| Run mode | Batch |
|--------------------------|-------|
| Time to start comparison | now |
| Notify at end of run | No |

1 match found in sequence:

catpasease : Chloramphenicol acetyltransferase (EC 2.3.1.28) (Xenobiotic
(from "var2sp.pep")
TOIG of: catl_pseae check: 491 from: 1 to: 212

| ID | CAT4_PSEAE | STANDARD; | PRT; | 212 AA. |
|----|--|-----------|------|---------|
| AC | P26841; Q9S542; | | | |
| DT | 01-AUG-1992 (Rel. 23, Created) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | |
| DT | 28-FEB-2003 (Rel. 41, Last annotation update) | | | |
| DE | Chloramphenicol acetyltransferase (EC 2.3.1.28) (Xenobiotic | | | |
| DE | acetyltransferase) (XAT). | | | |
| GN | CAT OR CATB7 OR PA0706. | | | |
| OS | Pseudomonas aeruginosa. | | | |
| OC | Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; | | | |
| OC | Pseudomonadaceae; Pseudomonas. | | | |
| OX | NCBI_TaxID=287; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A., AND CHARACTERIZATION. | | | |
| RC | STRAIN-PA0222; | | | |
| RX | MEDLINE=99290057; PubMed=10361706; | | | |
| RA | White P.A., Stokes H.W., Bunney K.L., Hall R.M.; | | | |
| RT | "Characterisation of a chloramphenicol acetyltransferase determinant | | | |
| RL | found in the chromosome of Pseudomonas aeruginosa."; | | | |
| RL | FEMS Microbiol. Lett. 175:27-35(1999). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN-ATCC 15692 / PA01; | | | |
| RX | MEDLINE=20437337; PubMed=10984043; | | | |
| RA | Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P., | | | |

| | |
|----|--|
| RA | Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., |
| RA | Garber R.L., Goltzy L., Tolentino E., Westbrook-Wedman S., Yuan Y., |
| RA | Brody L.L., Coulter S.N., Folger K.R., Kas A., Latis K., Lim R.M., |
| RA | Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., |
| RA | Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.; |
| RT | "Complete genome sequence of Pseudomonas aeruginosa PA01, an |
| RT | opportunistic pathogen."; |
| RL | Nature 406:959-964(2000). |
| RN | [3] |
| RP | SEQUENCE FROM N.A., AND CRYSTALLIZATION. |
| RC | STRAIN-ATCC 29260 / PA103; |
| RX | MEDLINE=97332513; PubMed=9188747; |
| RA | Tian Y., Beaman T.W., Roderick S.L.; |
| RT | "Purification and crystallization of Pseudomonas aeruginosa |
| RT | chloramphenicol acetyltransferase."; |
| RL | Protein 28:298-300(1997). |
| RN | [4] |
| RP | SEQUENCE OF 1-64 FROM N.A. |
| RC | STRAIN-ATCC 29260 / PA103; |
| RX | MEDLINE=88262583; PubMed=3133641; |
| RA | Hindahl M.S., Frank D.W., Hamood A., Iglewski B.H.; |
| RT | "Characterization of a gene that regulates toxin A synthesis in |
| RT | Pseudomonas aeruginosa."; |
| RL | Nucleic Acids Res. 16:5699-5699(1988). |
| RN | [5] |
| RP | X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS). |
| RC | STRAIN-ATCC 29260 / PA103; |
| RX | MEDLINE=98244846; PubMed=9578552; |
| RA | Beaman T.W., Sugantino M., Roderick S.L.; |
| RT | "Structure of the hexapeptide xenobiotic acetyltransferase from |
| RT | Pseudomonas aeruginosa."; |
| RL | Biochemistry 37:6689-6696(1998). |
| CC | -1- FUNCTION: THIS ENZYME IS AN EFFECTOR OF CHLORAMPHENICOL (CM) |
| CC | RESISTANCE IN BACTERIA. ACETYLATEDS CM BUT NOT 1-ACETOXY-CM. |
| CC | -1- CATALYTIC ACTIVITY: Acetyl-CoA + chloramphenicol = CoA + |
| CC | chloramphenicol 3-acetate. |
| CC | -1- SUBUNIT: Homotrimer. |
| CC | -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NOXI FAMILY OF |
| CC | ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4). |
| CC | -1- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 11 |
| CC | TO 37 DUE TO A FRAMESHIFT. |
| CC | ----- |
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| CC | or send an email to license@isb-sib.ch). |
| CC | ----- |
| DR | EMBL; AF036933; AAD02068.1; - |
| DR | EMBL; AE004506; AAG04095.1; - |
| DR | EMBL; X12366; -; NOT_ANNOTATED_CDS. |
| DR | PIR; C83557; C83557. |
| DR | PDB; 1XAT; 17-JUN-98. |
| DR | PDB; 2XAT; 17-JUN-98. |
| DR | InterPro; IPR001451; Hexapep_transf. |
| DR | PROSITE; PS00101; HEXAPEP_TRANSFERSSES; FALSE_NEG. |
| KW | Antibiotic resistance; Transferase; Acyltransferase; Repeat; |
| KW | 3D-structure; Complete proteome. |
| KW | ACT_SITE 79 |
| FT | CONFLICT 97 97 V -> A (IN REF. 3). |
| FT | CONFLICT 116 116 D -> E (IN REF. 3). |
| FT | CONFLICT 203 203 R -> Q (IN REF. 3). |
| FT | TURN 8 9 |
| FT | STRAND 12 13 |
| FT | TURN 15 17 |
| FT | TURN 21 22 |
| FT | STRAND 23 25 |
| FT | TURN 27 28 |
| FT | STRAND 30 32 |
| FT | HELIIX 34 36 |
| FT | HELIIX 40 43 |

```

FT STRAND 44 45
FT TURN 46 46
CC STRAND 57 59
FT STRAND 64 66
FT TURN 67 68
FT STRAND 70 72
FT TURN 75 78
FT TURN 81 82
FT HELIX 89 91
FT TURN 93 94
FT HELIX 96 98
FT STRAND 111 113
FT STRAND 118 119
FT TURN 121 122
FT STRAND 124 125
FT TURN 127 128
FT STRAND 130 131
FT TURN 133 134
FT STRAND 136 137
FT TURN 139 140
FT STRAND 142 143
FT STRAND 147 147
FT TURN 149 150
FT STRAND 151 154
FT TURN 155 158
FT STRAND 159 163
FT HELIX 167 176
FT HELIX 178 180
FT HELIX 183 193
FT TURN 194 194
FT HELIX 198 208
FT TURN 209 209
SQ SEQUENCE 212 AA; 23524 MW; 306E9F39978C19FC CRC64;

```

CAT4_PSEA Length: 212 July 16, 2003 13:42 Type: P Check: 491
 Found using 'var2' (kam816.key)

```

150 YAIAGGNARTIRKRFSDGDIQNLLEMAWMDPLADIAAPLCTGDIPLAAYKMKRO
-----|-----|
200 206

```

210 ATA

1 match found in sequence:

op65neigo ; Opacity protein OPA65 precursor (Fragment).
 (from 'Var2sp.pep')
 TOIG of: op65_neigo check: 3344 from: 1 to: 234

```

ID OP65_NEIGO STANDARD; PRT; 234 AA.
AC 004885;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA65 precursor (Fragment).
OS Neisseria gonorrhoeae.
CC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
CC Neisseriaceae; Neisseria.
OX NCBI_Taxid=485;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells."
RL EMBL J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.

```

```

CC -1- SUBCELLULAR LOCATION: Outer membrane.
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CC
DR EMBL; Z18940; CAI79373.1; -.
DR PIR; S36348; S36348.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.
FT NON_TER 1 1
FT SIGNAL <1 1 POTENTIAL.
FT CHAIN 2 >234 OPACITY PROTEIN OPA65.
FT NON_TER 234 234
SQ SEQUENCE 234 AA; 26242 MW; D66A0BA8424C2F1 CRC64;

```

OP65_NEIGO Length: 234 July 16, 2003 13:42 Type: P Check: 3344
 Found using 'var2' (kam816.key)

```

22 ITHDIPEPTGAKKAQSLTVSDYFRNIRTHSIHPRVSVGYDFGWRADYARYRKMKESN
-----|-----|
82 SSIKVTEDIKDKYKTEKTEHENGTFHAVVSLGISTIVDFQISDKI
72 78

```

1 match found in sequence:

Y002metja ; Hypothetical protein MJ0002.
 (from 'var2sp.pep')
 TOIG of: Y002_metja check: 316 from: 1 to: 243

```

ID Y002_METJA STANDARD; PRT; 243 AA.
AC Q60312;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0002.
GN MJ0002.
OS Methanococcus jannaschii.
CC Archaea; Euryarchaeota; Methanococci; Methanococcales;
CC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_Taxid=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RC MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Klenk H.-P., Roberts K.M., Hurst M.A., Kane B.P., Borodovsky M.,
RA Sultana G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Nguyen D.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kane B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -----
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-----
DR      EMBL; U67459; AAB97989.1; -.
DR      PIR; B64300; B64300.
DR      TIGR; M70002; -.
KW      Hypothetical protein; Complete proteome.
SQ      SEQUENCE 243 AA; 28492 MW; 2B1BE2C59F816CB9 CRC64;

Y002_METJA length: 243 July 16, 2003 13:42 Type: P Check: 316 ..
Found using 'var2' (kam816.key)

...

62      DFVSFELGKFLRELKPNANFIEIALSDKVLYSSKYHEDYKGIAYNCICRKLHHMKGFA
                                         |-----|
                                         112  118

122      KPLQKLCESYNNPKTLLIYLRAYYOGIICLSEGEFKSDPSSFRCL

...

-- Search Statistics --

Times:      CPU      Total Elapsed
            00:00:00.00      00:00:00.00

Number of sequences searched:      3
Number of sequence hits:      3
Number of separate matches:      3
Number of sequence hits saved:      0
```


> 0 <
01/10 Intelligenetics
> 0 <
Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "var2_spt" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.

Selected sequence key from "kam816.key":

var2 (AA) ID var2 AA preliminary pattern
1 followed by
2 a or k or g
2 l or r
2 y
2 k or r or h
2 k or r or h
2 wk

Selected files:

File : var2spt.pep

-- Output Parameters --

| Format Options: | File Options: | |
|-----------------------------|----------------------|-----|
| Nucleic acid code matching | Exact | No |
| Find non-matching hits only | Indirect file | No |
| Report key used | Sequence or key file | Yes |
| Note position of hit | List of hits | Yes |
| Display full annotations | Hit display | Yes |
| Sequence context | Name and annotations | Yes |

-- Run Parameters --

| Run mode | Batch |
|--------------------------|-------|
| Time to start comparison | now |
| Notify at end of run | NO |

1 match found in sequence:

097035 ; PLC-betaH1.
(from "var2spt.pep")
TOIG of: 097035 check: 1081 from: 1 to: 1012

ID 097035 PRELIMINARY; PRT; 1012 AA.
AC 097035;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PLC-betaH1.
OS Hydra magnipapillata (Hydra).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=105;
RA Koyanagi M., Ono K., Suga H., Iwabe N., Miyata T.;
RT "Phospholipase C cDNAs from sponge and hydra: Antiquity of genes
involved in the inositol phospholipid signaling pathway.";
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; AB017511; BAA76276.1; -
DR HSSP; P10688; 1DJX.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PL_PLC.
DR InterPro; IPR000909; PL_PLC_Xdom.
DR InterPro; IPR001711; PL_PLC_Y.
DR Pfam; PF00168; C2; 1.

DR Pfam; PF00388; PI-PLC-X; 1.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR ProDom; PD001202; PL_PLC_Y; 1.
DR SMART; SM00238; C2; 1.
DR SMART; SM00148; PLCXc; 1.
DR SMART; SM00149; PLCyc; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPIC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPIC_Y_DOMAIN; 1.
SQ SEQUENCE 1012 AA; 116186 MW; BD/CFF51F96A23118 CRC64;

097035 Length: 1012 July 16, 2003 13:43 Type: P Check: 1081
Found using 'var2' (kam816.key)

886 KRSQSISGLRLESPKQPIRRFTSPKLLGEDPTSSDYLRISGLSINTLKEHRLKKWKIKLF
936 942

946 DSDFLNLMOKAKGRIOCKRELEAKTKLLTLNLEKKNOLYRKIKTNF

1 match found in sequence:

g64146 ; Interleukin-3 receptor beta-subunit (Fragment).
(from "var2spt.pep")
TOIG of: g64146 check: 5352 from: 1 to: 896

ID 064146 PRELIMINARY; PRT; 896 AA.
AC 064146;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Interleukin-3 receptor beta-subunit (Fragment).
GN RIL-3R<BETA>.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370942; PubMed=7643220;
RA Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;
RT "Cloning of rat Interleukin-3 receptor beta-subunit from cultured
microglia and its mRNA expression in vivo.";
RT J. Neurosci. 15:5800-5809(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=Brain;
RA Gebicke-Haerter P.J.;
RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; S79263; AAB35068.1; -
DR EMBL; AJ000555; CAA04186.1; -
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR000282; CytoK_receptor_2.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003531; Hemtopoptn_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Signal.
FT NON_TER 1 1
FT 896 896
SQ SEQUENCE 896 AA; 99504 MW; 4C6E3B288A4A1052 CRC64;
064146 Length: 896 July 16, 2003 13:43 Type: P Check: 5352
Found using 'var2' (kam816.key)

```

421 PEKGLMSEMSNECTWTWDMPTLIVLIVLILFLLALRFGCIYCKIYRMKREKI
      |-----|
      471 477
481 PMSKSLRLQDGGKGLMPGSTVTTSSKNPTPOGPNILFSELQVGS
      .....
1 match found in sequence:
q8jt9 ; Hypothetical protein.
(from 'var2spt.pep')
TOIG of: q8jt9 check: 6954 from: 1 to: 437

ID Q8JT9 PRELIMINARY; PRT; 437 AA.
AC Q8JT9;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical protein.
GN LM054.
OS Lumpy skin disease virus (LSDV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Capripoxvirus.
OX NCBI_TaxID=59509;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Neethling vaccine LW 1959;
RA Kara P.D., Afonso C.L., Wallace D.B., Kutish G.F., Stipinovich C.,
RA Lu Z., Vreede F.T., Taljaard L.C.F., Zsak A., Viljoen G.J., Rock D.L.;
RT "Molecular characterization of the South African vaccine strain and
RT the field isolate of lumpy skin disease virus.";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF409138; AAN0279.1; -
KM Hypothetical protein.
SQ SEQUENCE 437 AA; 50521 MW; 500D63C6D9CC08EC CRC64;

Q8JT9 Length: 437 July 16, 2003 13:43 Type: P Check: 6954
Found using 'var2' (kam816.key)

274 IIRNRSKETDRIYINAEKIHIFINRYSCINESIYNEVPESITVQEFISALYHKKEED
      |-----|
      324 330
334 DSLKGISLCSLICVLPKKDKIKNEISKLCNIINNSNKKSLNN
      .....
1 match found in sequence:
q8v3p3 ; SPV051 hypothetical protein.
(from 'var2spt.pep')
TOIG of: q8v3p3 check: 8140 from: 1 to: 439

ID Q8V3P3 PRELIMINARY; PRT; 439 AA.
AC Q8V3P3;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE SPV051 hypothetical protein.
GN SPV051.
OS Swinepox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Sulpoxvirus.
OX NCBI_TaxID=10276;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17077-99;
RX MEDLINE=21624277; PubMed=11752168;
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Osorio F.A., Balinsky C.,
RA Kutish G.F., Rock D.L.;

```

```

RT "The genome of swinepox virus.";
RL J. Virol. 76:783-790(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=17077-99;
RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C., Osorio F.A., Zsak L.,
RA Kutish G.F., Rock D.L.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF410153; AAL69790.1; -
KM Hypothetical protein.
SQ SEQUENCE 439 AA; 50984 MW; 4991293795FE3850 CRC64;

Q8V3P3 Length: 439 July 16, 2003 13:43 Type: P Check: 8140
Found using 'var2' (kam816.key)

275 VRNYTKSTDKYINVOEIIDFKYSSSDSVSNFLPERCVTIQEFMFSAIYKMKTFD
      |-----|
      325 331
335 DTLRGVSLCSLICISPKKAISNDIDILCKIINKNKKNDIIN
      .....
1 match found in sequence:
q91mw3 ; LSDV054 hypothetical protein.
(from 'var2spt.pep')
TOIG of: q91mw3 check: 7600 from: 1 to: 437

ID Q91MW3 PRELIMINARY; PRT; 437 AA.
AC Q91MW3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE LSDV054 hypothetical protein.
GN LSDV054 OR LD054.
OS Lumpy skin disease virus (LSDV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Capripoxvirus.
OX NCBI_TaxID=59509;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Neethling 2490;
RX MEDLINE=21329495; PubMed=11435593;
RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "Genome of lumpy skin disease virus.";
RL J. Virol. 75:7122-7130(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Neethling 2490;
RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Neethling Warmbaths LW;
RA Kara P.D., Afonso C.L., Wallace D.B., Kutish G.F., Stipinovich C.,
RA Lu Z., Vreede F.T., Taljaard L.C.F., Zsak A., Viljoen G.J., Rock D.L.;
RT "Molecular characterization of the South African vaccine strain and
RT the field isolate of lumpy skin disease virus.";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF325528; AAK85015.1; -
KM EMBL: AF409137; AAN02622.1; -
SQ SEQUENCE 437 AA; 50555 MW; 2F9798DBC80C223F CRC64;

Q91MW3 Length: 437 July 16, 2003 13:43 Type: P Check: 7600
Found using 'var2' (kam816.key)

```

274 IIRNTRKNDTRYNAEKIIHFINKYSCINESIYNEVPPESTIVQEFISALYHKWKED 324 330
 334 DSLKIGISLCCLICVLKPKDKIKRNEISKLCNIINNDSNKKSSLNN

 1 match found in sequence:
 q9df11 : Doublesex-like protein Dmrt11 (Fragment).
 (from "var2spt.pep")
 Toig of: q9df11 check: 8097 from: 1 to: 31

ID Q9DF11 PRELIMINARY; PRT; 31 AA.
 AC Q9DF11;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
 DE Doublesex-like protein Dmrt11 (Fragment).
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang X., Zhou R.;
 RT "A conserved family of doublesex related genes from fish.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF272963; AAC18559.1;
 DR InterPro: IPR001275; DM_DNA-binding.
 DR Pfam: PF00751; DM-domain; 1.
 FT NON_TER 1 1
 FT 31 31
 SQ SEQUENCE 31 AA; 3734 MW; 211519BE4019B92D CRC64;

Q9DF11 Length: 31 July 16, 2003 13:43 Type: P Check: 8097 ..
 Found using 'var2' (kam816.key)

1 |-----|
 VVSALKGHKRYRWKDCMVCVCTLIARQRY
 9 15

-- Search Statistics --

| Times: | CPU | Total Elapsed |
|--------------------------------|-------------|---------------|
| | 00:00:00.00 | 00:00:00.00 |
| Number of sequences searched: | | 6 |
| Number of sequence hits: | | 6 |
| Number of separate matches: | | 6 |
| Number of sequence hits saved: | | 0 |

1

> 0 <
01/0 Intelligenetics
> 0 <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "var3_pir" --

Selected search type is key against sequence data banks or files.

Selected scope is sequence. "kam816.key";

Selected sequence key from "var3_pir.key";

1 var3 (AA) ID var3 AA preliminary pattern
followed by
2 a or k or g
2 1 or r
2 y
2 k or r or h
2 k or r or h
2 l f

Selected files:

File : var3pir.pep

-- Output Parameters --

Format Options: File Options:
Nucleic acid code matching Exact Indirect file NO
Find non-matching hits only No Sequence or key file NO
Report key used Yes List of hits Yes
Note position of hit Yes Hit display Yes
Display full annotations Yes Name and annotations Yes
Sequence context 50

-- Run Parameters --

Run mode Batch
Time to start comparison now
Notify at end of run No

1 match found in sequence:

c82922 ; TOIG of: c82922 check: 8625 from: 1 to: 521
(from "var3pir.pep")

TOIG of: c82922 check: 8625 from: 1 to: 521

P1:c82922 - methionyl-tRNA synthetase U0197 [imported] - Ureaplasma urealyticum

C:Species: Ureaplasma urealyticum

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Feb-2003

C:Accession: C82922

R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell,

G.H.

Submitted to GenBank, February 2000

A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views
of a minimal genome and sexually transmitted pathogen.

A:Reference number: A82870

A:Accession: C82922

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-521 <GUA>

A:Cross-references: GB:AE002119; GB:AF222894; NID:g6899153; PIDN:AAF30604.1;

GSDB:GM00123; UOSP:U0197

A:Experimental source: serovar 3; biovar 1

C:Genetics:

A:Gene: mets: U0197

A:Genetic code: SGC3

C:Superfamily: methionyl-tRNA synthetase

C82922 Length: 521 July 16, 2003 13:44 Type: P Check: 8625 ..
Found using 'vars' (kam816.key)

1 MLKKKFFISPIPIYSSGNHGHATTITADYAKRKLFGDVFLLTGMDEHGCKIOO
35 41

61 KAFENISPRALVDNRNSIIFLMLKRLNISF

1 match found in sequence:
g64691 ; TOIG of: g64691 check: 6636 from: 1 to: 270
(from "var3pir.pep")
TOIG of: g64691 check: 6636 from: 1 to: 270

P1:g64691 - UDP-N-acetylglucosamine acyltransferase - Helicobacter pylori
(strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 18-Jun-1999

C:Accession: G64691

R:Tombs, J.F.; White, O.; Kervavage, A.R.; Clayton, R.A.; Sutton, G.G.;

Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.;

Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus,

B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.;

Fitzgerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne,

J.D.; Uitterlinden, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Meldman,

J.M.; Fujii, C.; Bowman, C.; Watney, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.;

Fraser, C.M.; Venter, J.C.

A:Title: The complete genome sequence of the gastric pathogen Helicobacter

pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: G64691

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-270 <TOM>

A:Cross-references: GB:AE000637; GB:AE000511; NID:g2314536; PIDN:AAD08418.1;

PID:g2314545; TIGR:HP1375

C:Superfamily: UDP-N-acetylglucosamine acyltransferase

664691 Length: 270 July 16, 2003 13:44 Type: P Check: 6636 ..
Found using 'vars' (kam816.key)

162 AKCGTAGSALGKDVPPCYVEGNRAFTIRGLNRHRRHROLLESKDIDFYALYKRLFRPI
212 218

222 PSLRESAKLELEHANNPNPVKEICSFILSSNGVAKSSEYSSEKQ
212 218

1 match found in sequence:

g71826 ; TOIG of: g71826 check: 5582 from: 1 to: 270
(from "var3pir.pep")

TOIG of: g71826 check: 5582 from: 1 to: 270

P1:g71826 - udp-n-acetylglucosamine acyltransferase - Helicobacter pylori
(strain J99)

C:Species: Helicobacter pylori

A:Variety: strain J99

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 18-Jun-1999

C:Accession: G71826

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;

Smith, D.R.; Noonan, B.; Guild, B.C.; deJonghe, B.L.; Carmel, G.; Tummino, P.J.;

Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.;

Mills, S.D.; Jiang, O.; Taylor, D.E.; Voris, G.F.; Trust, T.J.

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human

gastric pathogen Helicobacter pylori.

A:Reference number: A71800; MUID:99120557; PMID:9923682

```

A:Accession: G71826
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-270 <ARN>
A:Cross-references: GB:AE001551; GB:AE001439; NID:94155887; PIDN:AAD06863.1;
PID:94155893
A:Experimental source: strain J99
C:Genetics:
A:Gene: lpxA
C:Superfamily: UDP-N-acetylglucosamine acyltransferase

71826 Length: 270 July 16, 2003 13:44 Type: P Check: 5582 ..
Found using 'var3' (kam816.key)

...

162 AKGCMAGKALGKDVPPYCTVEGNRAFRGLNRHRMQLLESKDIDFIHALYKRLFRPI
|-----|
212 218

222 PSRESAKLELEHANNPFVKETCSFILESSRGVAYKSSEYSSEKO

...

1 match found in sequence:
h72742 : TOIG of: h72742 check: 4517 from: 1 to: 172
(from "var3pir.pep")
TOIG of: h72742 check: 4517 from: 1 to: 172

PI: H72742 - hypothetical protein APE0472 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 08-Sep-2000
C:Accession: H72742
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no,
K.; Takahashi, M.; Sekine, M.; Baba, S.; Ankai, A.; Kosugi, H.; Hosoyama, A.;
Fukui, S.; Nagai, Y.; Nishijima, K.; Nakazawa, H.; Takamiya, M.; Masuda, S.;
Fukunishi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, T.; Kushida, N.; Oguchi, A.;
Aoki, K.; Kubota, K.; Nakamura, Y.; Nomura, N.; Sako, Y.; Kikuchi, H.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic
Crenarchaeon, Aeropyrum pernix K1
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: H72742
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-172 <KAN>
A:Cross-references: DDBJ:AP000059; NID:95103911; PIDN:BA79436.1; PID:01043222;
PID:95104120
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0472
C:Superfamily: Aeropyrum pernix hypothetical protein APE0472

H72742 Length: 172 July 16, 2003 13:44 Type: P Check: 4517 ..
Found using 'var3' (kam816.key)

...

114 TALSLEAPLWTEDEKALIRASFNSLYVALDTESEVNLHGEPLESTREKLYKLEFQ
|-----|
164 170

1 match found in sequence:
t27570 : TOIG of: t27570 check: 7198 from: 1 to: 721
(from "var3pir.pep")
TOIG of: t27570 check: 7198 from: 1 to: 721

PI: T27570 - hypothetical protein ZC434.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T27570

...

R:Wilkinson, J.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z20388
A:Accession: T27570
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-721 <MIL>
A:Cross-references: EMBL:Z75714; PIDN:CAB00063.1; GSPDB:GN00019; CESP:ZC434.6
A:Experimental source: clone ZC434
C:Genetics:
A:Gene: CESP:ZC434.6
A:Map position: 1
A:Introns: 49/1; 244/2; 357/2; 440/2; 524/3; 611/3; 699/1
C:Superfamily: Caenorhabditis elegans hypothetical protein ZC434.6

T27570 Length: 721 July 16, 2003 13:44 Type: P Check: 7198 ..
Found using 'var3' (kam816.key)

...

500 AIIAAADYGVETDEVAKVDKLLITTFDCLITSNFWFDDCFMOKLDGGRHKLFPNSY
|-----|
550 556

560 GFNOKSTYISMESHAPPTVLMWLTIFALGSDKETLVNKSCKSHL

...

1 match found in sequence:
t41055 : TOIG of: t41055 check: 5944 from: 1 to: 1315
(from "var3pir.pep")
TOIG of: t41055 check: 5944 from: 1 to: 1315

PI: T41055 - membrane ATPase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T41055
R:Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, August 1998
A:Reference number: Z21967
A:Accession: T41055
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1315 <HIL>
A:Cross-references: EMBL:AL031324; PIDN:CAA20449.1; GSPDB:GN00068;
SPDB:SPCC1672.11c
A:Experimental source: strain 972h-; cosmid c1672
C:Genetics:
A:Gene: SPDB:SPCC1672.11c
A:Map position: 3

T41055 Length: 1315 July 16, 2003 13:44 Type: P Check: 5944 ..
Found using 'var3' (kam816.key)

...

1251 SKSPONLIFAGVITYLLAASGONYIFISMTNFISHLNRLNRRYVSKKYLKFLFADL
|-----|
1301 1307

1311 QNECV

1 match found in sequence:
t49926 : TOIG of: t49926 check: 7827 from: 1 to: 397
(from "var3pir.pep")
TOIG of: t49926 check: 7827 from: 1 to: 397

PI: T49926 - hypothetical protein F1714.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Mar-2001
C:Accession: T49926

```

R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.;
 Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24490

A:Accession: T49926

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-397 <BEV>

A:Cross-references: EMBL:AL353994; GSPDB:GN00063; ATSP:F17I14.90

A:Experimental source: cultivar Columbia; BAC clone F17I14

C:Genetics:

A:Gene: ATSP:F17I14.90

A:Map position: 5

A:Introns: 76/3; 86/3; 124/1; 164/3; 198/3; 315/3; 330/3; 369/3

C:Superfamily: Arabidopsis thaliana hypothetical protein F17I16.20

749926 Length: 397 July 16, 2003 13:44 Type: P Check: 7827 ..

Found using 'var3' (kam816.key)

...

339 SICVSVSVVVGILGMNIPFPWNKKHMKWVSGTATVCAILFVIIMSFARVKKLFGF

389 395

-- Search Statistics --

Times: CPU Total Elapsed

00:00:00.00 00:00:00.00

Number of sequences searched: 7

Number of sequence hits: 7

Number of separate matches: 7

Number of sequence hits saved: 0

6

1

ATC9_SCHPO Length: 1315 July 16, 2003 13:45 Type: P Check: 5944 ..
Found using 'var3' (kam816.key)

1251 SKSPONFLIFAGVYIYLLAASGQNTIFISMTNFIISHLNNRLNRRYVSKLIRLADL
1301 1307

1311 ONEGV

1 match found in sequence:
lpkxhelp; Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase
(from "var3sp.pep")
TOIG of: lpkx_help check: 5582 from: 1 to: 270

ID LPXA_HELPY STANDARD; PRT; 270 AA.
AC Q9ZJL7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase
(EC 2.3.1.129) (UDP-N-acetylglucosamine acyltransferase).
GN LPXA OR HPI1289.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -1- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF LIPID A, A
PHOSPHORYLATED GLYCOLIPID THAT ANCHORS THE LIPOLYSACCHARIDE TO
THE OUTER MEMBRANE OF THE CELL (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxytetradecanoyl-[acyl-carrier
protein] + UDP-N-acetylglucosamine -> [acyl-carrier protein] +
UDP-3-O-(3-hydroxytetradecanoyl)-N-acetylglucosamine.
CC -1- PATHWAY: Lipid A biosynthesis; first step.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TRANSFERASE HEXAPEPTIDE REPEAT FAMILY.
CC LPXA SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE001551; AAD06863.1; -
CC PIR: G71826; G71826.
CC HSSP: P10440; 1LXA.
CC HAMAP: MF_00387; -; 1.
CC InterPro: IPR001451; Hexapep_transf.
CC Pfam: PF00132; hexapep; 7.
CC PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 2.
CC Transferrase; Acyltransferase; Lipid A biosynthesis; Lipid synthesis;
KW Repeat; Complete proteome
SQ SEQUENCE 270 AA; 29790 MW; EC72E581E0226E23 CMC64;
LPXA_HELPY Length: 270 July 16, 2003 13:45 Type: P Check: 5582 ..

Found using 'var3' (kam816.key)

162 AKCGMIAGKSALGKDVPCYVEGNRAPIRGLNRHRMRLLESKDIDFTHALYKRLFRPI
212 218

222 PSLRESAKLELEBHANNPFVKEICFISLESKGVAKSSEYSSEKQ

1 match found in sequence:
lpkxhelp; Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase
(from "var3sp.pep")
TOIG of: lpkx_help check: 6636 from: 1 to: 270

ID LPXA_HELPY STANDARD; PRT; 270 AA.
AC Q25927;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase
(EC 2.3.1.129) (UDP-N-acetylglucosamine acyltransferase).
GN LPXA OR HPI1375.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=26695; ATCC 700392;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khairat H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Matheny L., Mallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
pylori.";
RL Nature 388:539-547(1997).
CC -1- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF LIPID A, A
PHOSPHORYLATED GLYCOLIPID THAT ANCHORS THE LIPOLYSACCHARIDE TO
THE OUTER MEMBRANE OF THE CELL (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxytetradecanoyl-[acyl-carrier
protein] + UDP-N-acetylglucosamine -> [acyl-carrier protein] +
UDP-3-O-(3-hydroxytetradecanoyl)-N-acetylglucosamine.
CC -1- PATHWAY: Lipid A biosynthesis; first step.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TRANSFERASE HEXAPEPTIDE REPEAT FAMILY.
CC LPXA SUBFAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE000637; AAD08418.1; -
CC PIR: G64691; G64691.
CC HSSP: P10440; 1LXA.
CC TIGR: HPI1375; -
CC HAMAP: MF_00387; -; 1.
CC InterPro: IPR001451; Hexapep_transf.
CC Pfam: PF00132; hexapep; 8.

DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 KW Transferase: Acyltransferase; Lipid A biosynthesis; Lipid synthesis;
 KW Repeat: Complete proteome.
 SO SEQUENCE 270 AA; 2985 MW; 3668D2ED24BBA4E CRC64;
 LPXA_HELPY Length: 270 July 16, 2003 13:45 Type: P Check: 6636 ..
 Found using 'var3' (kam816.key)

162 AKGCMIAKSAIGKDPVPPYCTVEGNRAFRGLNRRHRMQLLESKDIDPIYALKLFPRI
 212 218
 PSLRESAKLELEHANPVEKICFILESNGVAKSSEYSEKRO

222

1 match found in sequence:
 nicacaeel; Nicastatin homolog precursor.
 (from "var3sp.pep")
 TOIG of: nicacaeel check: 7198 from: 1 to: 721

ID NICA_CAEEL STANDARD; PRT; 721 AA.
 AC Q23316;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE Nicastatin homolog precursor.
 GN APH-2 OR ZC434.6.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RX [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN-Bristol N2;
 RA Wilkinson J.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP REVISIONS.
 RP Jones S.J.M.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP POSSIBLE FUNCTION, AND GENE NAME.
 RX MEDLINE=20445163; PubMed=10993067;
 RA Yu G., Nishimura M., Atawaka S., Levitan D., Zhang L., Tandon A.,
 RA Song Y.-Q., Rogava E., Chen F., Kawarai T., Supala A., Levesque L.,
 RA Xu D.H., Yang D.-S., Holmes E., Milman P., Liang Y., Zhang D.M.,
 RA Xu D.H., Sato C., Rogava E., Smith M., Janus C., Zhang Y.,
 RA Aebersold R., Farrer L.S., Sorbi S., Bruni A., Fraser P.E.,
 RA St George-Hyslop P.H.;
 RT "Nicastatin modulates presenilin-mediated notch/glp-1 signal
 transduction and betaAPP processing.";
 RL Nature 407:48-54(2000).
 CC -1- FUNCTION: PLAYS A ROLE IN EMBRYONIC GLP-1 SIGNALING.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).
 CC -1- SIMILARITY: BELONGS TO THE NICASTRIN FAMILY.

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CC EMBL: Z75714; CAB00063.1; -
 DR PIR: T27570; T27570.
 DR Trmpep: ZC434.6; CE15229.
 KW Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 721
 FT DOMAIN 17 678
 FT TRANSMEM 679 699
 FT DOMAIN 700 721
 FT CARBOHYD 40 40
 FT CARBOHYD 181 181
 FT CARBOHYD 271 271
 FT CARBOHYD 328 328
 FT CARBOHYD 409 409
 FT CARBOHYD 625 625
 SO SEQUENCE 721 AA; 81383 MW; 904063F6E9CFBD1 CRC64;
 Found using 'var3' (kam816.key)

500 NICA_CAEEL Length: 721 July 16, 2003 13:45 Type: P Check: 7198 ..
 Found using 'var3' (kam816.key)

500 AIIAAADYGVETDEVAVAKDKKLTITTFDCLITSNFWDCDFMOKLDGRGRHKLFNSY
 530 536

560 GFNOKSTYISMESHAPPTVLHMLTIFALGSDKXETLVNYSKSCSHL

1 match found in sequence:
 symurepa; Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
 (from "var3sp.pep")
 TOIG of: sym_urepa check: 8625 from: 1 to: 521

ID SYM_UREPA STANDARD; PRT; 521 AA.
 AC Q9P0U6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
 DE (METS).
 GN METG OR METS OR U0197.
 OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
 CC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
 OX NCBI_TaxID=134821;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Serovar 3;
 RX MEDLINE=20500219; PubMed=11048724;
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
 RA Cassell G.H.;
 RT "The complete sequence of the mucosal pathogen Ureaplasma
 urealyticum.";
 RL Nature 407:757-762(2000).
 CC -1- FUNCTION: IS required not only for elongation of protein synthesis
 CC but also for the initiation of all mRNA translation through
 CC initiator tRNA(fMet) aminoacylation (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
 CC diisophosphate + L-methionyl-tRNA(Met).
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
 CC Metc subfamily 2A.

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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).

CC EMBL: AE002119; AAF30604.1; -
 DR HSSP: P23395; 1A8H.
 DR HAMAP: MF_01228; -; 1.

DR InterPro: IPR002300; tRNA-synt_1a.
 DR InterPro: IPR001412; tRNA-synt_1.
 DR InterPro: IPR002304; tRNA-synt_met.
 DR Pfam: PF00133; tRNA-synt_1; 2.
 DR PRINTS: PRO1041; TRNASYNTHMET.
 DR TIGRFAMs: TIGR00398; metg; 1.
 DR PROSITE: PS00178; AA.TRNA.LIGASE.I; FALSE NEG.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Metal-binding; Zinc; Complete proteome.
 FT SITE 14 24 "HIGH" REGION.
 FT SITE 306 310 "KMSKS" REGION.
 FT METAL 129 129 ZINC (BY SIMILARITY).
 FT METAL 132 132 ZINC (BY SIMILARITY).
 FT METAL 151 151 ZINC (BY SIMILARITY).
 FT METAL 155 155 ZINC (BY SIMILARITY).
 FT BINDING 309 309 ATP (BY SIMILARITY).
 SQ SEQUENCE 521 AA; 60830 MW; F9CD1A428B132DC5 CRC64;

SYM UREPA length: 521 July 16, 2003 13:45 Type: P Check: 8625 ..
 Found using 'var3' (kam816.key)

1 MLKQKFFISTPIYYSGNPHIGHAYTTIADVLARYKRLFGYDVFPLTGMDHGORIQ
 35 41

61 KAFENISPKALVDNRNSIIFLNKRLNISE

...

-- Search Statistics --

| Times: | CPU | Total Elapsed |
|--------|-------------|---------------|
| | 00:00:00.00 | 00:00:00.00 |

| | |
|--------------------------------|---|
| Number of sequences searched: | 5 |
| Number of sequence hits: | 5 |
| Number of separate matches: | 5 |
| Number of sequence hits saved: | 0 |

> 0 <
01 10 Intelligenetics
> 0 <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "var3_spt" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence. "kam816.key";

Selected sequence key from "kam816.key";

var3 (AA) ID var3 AA preliminary pattern

Followed by

1 a or k or g

2 1 or r

2 y or r or h

2 k or r or h

2 If

Selected files:

File : var3spt.pep

-- Output Parameters --

Format Options:

| Nucleic acid code matching | Exact | Indirect file | NO |
|-----------------------------|-------|----------------------|-----|
| Find non-matching hits only | No | Sequence or key file | No |
| Report key used | Yes | List of hits | No |
| Note position of hit | Yes | Hit display | Yes |
| Display full annotations | Yes | Name and annotations | Yes |
| Sequence context | 50 | | Yes |

-- Run Parameters --

| Run mode | Batch |
|--------------------------|-------|
| Time to start comparison | now |
| Notify at end of run | No |

1 match found in sequence:

q8h1g7 ; MRS2-8.

(from "var3spt.pep")

TOIG of: q8h1g7 check: 8275 from: 1 to: 380

| ID | Q8H1G7 | PRELIMINARY | PRT | 380 AA |
|----|---|-------------|-----|--------|
| AC | Q8H1G7 | | | |
| DT | 01-MAR-2003 (TREMBlrel. 23, Created) | | | |
| DT | 01-MAR-2003 (TREMBlrel. 23, Last sequence update) | | | |
| DT | 01-MAR-2003 (TREMBlrel. 23, Last annotation update) | | | |
| DE | MRS2-8. | | | |
| OS | MRS2-8. | | | |
| OS | Arabidopsis thaliana (Mouse-ear cross). | | | |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | | |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; | | | |
| OC | eurosid II; Brassicales; Brassicaceae; Arabidopsis. | | | |
| OX | NCBI_TaxID=3702; | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RP | MDLINE=21624993; PubMed=11752386; | | | |
| RA | Li L., Tutone A.F., Drummond R.S.M., Gardner R.C., Luan S.; | | | |
| RT | "A novel family of magnesium transport genes in Arabidopsis."; | | | |
| RL | Plant Cell 13:2761-2775(2001). | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Gardner R.C., Drummond R.S.M.; | | | |
| RL | Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL: AY150293; AAN73218.1; - | | | |
| SO | SEQUENCE 380 AA; 42912 MW; 51E0E0EF85840F8 CRC64; | | | |

Q8H1G7 Length: 380 July 16, 2003 13:46 Type: P Check: 8275 ..
Found using 'var3' (kam816.key)

322 SICVSVSVVVGILGNIPFPNKKHMKWVSGTATVCAILFVTIMSRARKKLFGF
372 378

1 match found in sequence:

q814p8 ; Hypothetical protein.

(from "var3spt.pep")

TOIG of: q814p8 check: 9498 from: 1 to: 179

| ID | Q814P8 | PRELIMINARY | PRT | 179 AA |
|----|--|-------------|-----|--------|
| AC | Q814P8 | | | |
| DT | 01-MAR-2003 (TREMBlrel. 23, Created) | | | |
| DT | 01-MAR-2003 (TREMBlrel. 23, Last sequence update) | | | |
| DT | 01-MAR-2003 (TREMBlrel. 23, Last annotation update) | | | |
| DE | Hypothetical protein. | | | |
| GN | PFL2595W. | | | |
| OS | Plasmodium falciparum (isolate 3D7). | | | |
| OC | Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. | | | |
| OX | NCBI_TaxID=36329; | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RP | STRAIN=3D7; | | | |
| RC | MDLINE=22255705; PubMed=12368864; | | | |
| RA | Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., | | | |
| RA | Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., | | | |
| RA | Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., | | | |
| RA | Chan M.-S., Nene V., Shallow S.J., Sun B., Peterson J., Angiuoli S., | | | |
| RA | Perle M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., | | | |
| RA | McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., | | | |
| RA | Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., | | | |
| RA | Fraser C.M., Barrell B.; | | | |
| RT | "Genome sequence of the human malaria parasite Plasmodium | | | |
| RT | falciparum."; | | | |
| RL | Nature 419:498-511(2002). | | | |
| DR | EMBL: AE014852; AAN36601.1; - | | | |
| KW | Hypothetical protein. | | | |
| SO | SEQUENCE 179 AA; 20824 MW; 58981BC75546B4C4 CRC64; | | | |

Q814P8 Length: 179 July 16, 2003 13:46 Type: P Check: 9498 ..
Found using 'var3' (kam816.key)

1 match found in sequence:

q8ksr8 ; Waad.

(from "var3spt.pep")

TOIG of: q8ksr8 check: 4841 from: 1 to: 336

| ID | Q8KSR8 | PRELIMINARY | PRT | 336 AA |
|----|---|-------------|-----|--------|
| AC | Q8KSR8 | | | |
| DT | 01-OCT-2002 (TREMBlrel. 22, Created) | | | |
| DT | 01-OCT-2002 (TREMBlrel. 22, Last sequence update) | | | |
| DT | 01-MAR-2003 (TREMBlrel. 23, Last annotation update) | | | |
| DE | Waad. | | | |
| GN | WAAJ. | | | |
| OS | Salmonella enterica subsp. arizonae. | | | |
| OC | Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; | | | |
| OC | Enterobacteriaceae; Salmonella. | | | |
| OX | NCBI_TaxID=59203; | | | |

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SARC 5;
RA Kaniuk N.A., Monteiro M.A., Parker C.T., Whitfield C.;
RT "Molecular diversity of the genetic loci responsible for
RT lipopolysaccharide core oligosaccharide assembly within the genus
RT Salmonella";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF511116; AAA48163.1;
SQ SEQUENCE 336 AA; 38891 MW; 87E86B135325BDAL CRC64;

08KSR8 Length: 336 July 16, 2003 13:46 Type: P Check: 4841
Found using 'var3' (kam816.key)

257 NTIIHYGATKPMHMANVPSYIYRNARLNSPKDFPGKDARTIVEFKRKHLFVQG
307 313
317 HYFKGLAGSAVLYRKVPHK

-----
1 match found in sequence:
q8p6w5 : Cytochrome B561.
(from "var3spt.pep")
Total of: q8p6w5 check: 2337 from: 1 to: 187

ID Q8P6W5 PRELIMINARY; PRT; 187 AA.
AC Q8P6W5;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cytochrome B561.
GN YODB OR KXC2850.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_Taxid=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 33913 / NCPPB 528;
RA MEDLINE-22022145; PubMed-12024217;
RA da Silva A.C.R., Ferro J.A., Relnach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Canargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergro F., Ciapina L.P.,
RA Clearelli R.M.B., Coutinho L.U., Cursino-Santos J.R., El-Dorriy H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Loceli E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Sphola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
DR EMBL; AE012398; AAA42122.1;
DR InterPro: IPR000516; N1_hydr_CyTB.
DR Pfam: PF01292; N1_hydr_CyTB; 1.
KW Complete proteome.
SQ SEQUENCE 187 AA; 21077 MW; 423897EBC8C7DD560 CRC64;

08P6W5 Length: 187 July 16, 2003 13:46 Type: P Check: 2337
Found using 'var3' (kam816.key)

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112 TSGLRPRFWGFLFNVPKLSAPDEQLRAVSHVHEWGFLLIAVLAVLAHGAALYHHLFQRD
162 168
172 ATLTRMLPRGWLSPKX

-----
1 match found in sequence:
q8qne6 : Esv-1-133.
(from "var3spt.pep")
Total of: q8qne6 check: 9763 from: 1 to: 353

ID Q8QNE6 PRELIMINARY; PRT; 353 AA.
AC Q8QNE6;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Esv-1-133.
OS Ectocarpus siliculosus virus.
OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
OX NCBI_Taxid=37665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Esv-1;
RA Delaroque N., Bothe G., Pohl T., Knippers R., Mueller D.G., Boland W.;
RT "The complete nucleotide sequence of the Ectocarpus siliculosus virus
RT genome";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF204951; AAK14551.1;
SQ SEQUENCE 353 AA; 39951 MW; 87151E1BD44D094 CRC64;

Q8QNE6 Length: 353 July 16, 2003 13:46 Type: P Check: 9763
Found using 'var3' (kam816.key)

76 DMPDAIDMETANGVMSINDADKMGARLNMATSRLEKRGFEVNDPAGYKYLFLK
126 132
136 FIYNHLEVYSKRNITYQAAYVDPATYVRAVLCFWQIISFAALMKE

-----
1 match found in sequence:
q8vqg9 : ORF43.
(from "var3spt.pep")
Total of: q8vqg9 check: 3014 from: 1 to: 720

ID Q8VQ9 PRELIMINARY; PRT; 720 AA.
AC Q8VQ9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE ORF43.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TY4;
RA MEDLINE-21562640; PubMed-11705958;
RA Yamaguchi T., Hayashi T., Takami H., Ohnishi M., Murata T.,
RA Nakayama K., Asakawa K., Ohara M., Komatsuzawa H., Sugai M.;
RT "Complete Nucleotide Sequence of a Staphylococcus aureus Exfoliative
RT toxin B Plasmid and Identification of a Novel ADP-Ribosyltransferase,
RT EDIN-C";
RL Infect. Immun. 69:7760-7771(2001).
DR EMBL; AP003088; BAB78441.1;
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001140; ABC_TM_transporter.
DR InterPro: IPR003439; ABC_transporter.

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DR InterPro: IPR005074; Peptidase_C39.
DR Pfam: PF00064; ABC_membrane_1.
DR Pfam: PF00005; ABC_tran_1.
DR Pfam: PF03412; Peptidase_C39; 1.
DR Prodom: PD000006; ABC_transporter_1.
DR SMART: SM00382; AAA; 1.
DR ATP-binding: Plasmid.
DR SEQUENCE 720 AA; 81680 MW; 4B1A3AD3C3C591CA CRC64;
SQ
ORVYQ9 Length: 720 July 16, 2003 13:46 Type: P Check: 3014
Found using 'var3' (Kam816.key)

714 FKKEGCV
-----
1 match found in sequence:
q9dwd8 : PR52.
(from "var3spt.pep")
TOIG of: q9dwd8 check: 2812 from: 1 to: 530

ID Q9DWD8 PRELIMINARY; PRT; 530 AA.
AC Q9DWD8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PR52.
GN R52.
OS Rat cytomegalovirus (strain Mastricht).
OC Viruses; dsDNA viruses; no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Mutomegalovirus.
OX NCBI_TaxID=79700;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mastricht;
RX MEDLINE=20366325; PubMed=10906222;
RT "Vink C., Beuken E., Bruggeman C.A.;
RT "Complete DNA sequence of the rat cytomegalovirus genome.";
RL J. Virol. 74:7656-7665(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Mastricht;
RX MEDLINE=20473137; PubMed=11018281;
RT Gruijthuisen Y.K., Beuken E., Bruggeman C.A., Vink C.;
RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a
RT spliced transcript.";
RL Virus Res. 69:119-130(2000).
DR EMBL: AF232689; AAF99151.1; -.
DR InterPro: IPR002597; Herpes_env.
DR Pfam: PF01673; Herpes_env; 1.
DR SEQUENCE 530 AA; 60538 MW; 1F9BAA2A685CA744 CRC64;
SQ
Q9DWD8 Length: 530 July 16, 2003 13:46 Type: P Check: 2812
Found using 'var3' (Kam816.key)

375 LDLPADLKNKDLSSYLADAEPAKATPPGSRDPFELDATTYLLRGVGVGLKHLFTDP
-----1
425 431
435 VCAANIRATDTSVLFEDVPMNYLNEVKLAICSTNAIPSAVERDFWL
-----
1 match found in sequence:
q9lxd5 : Hypothetical 44.8 kDa protein.

```

```

(from "var3spt.pep")
TOIG of: q9lxd5 check: 7827 from: 1 to: 397

ID Q9LXD5 PRELIMINARY; PRT; 397 AA.
AC Q9LXD5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 44.8 kDa protein.
GN F1714_90.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Beyan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL353994; CAB89358.1; -.
DR InterPro: IPR002523; Mg2+-transptCorA.
DR Pfam: PF01544; CorA; 1.
DR Hypothetical protein.
SQ SEQUENCE 397 AA; 44752 MW; 496F484DD659E4A2 CRC64;
q9lxd5 Length: 397 July 16, 2003 13:46 Type: P Check: 7827
Found using 'var3' (Kam816.key)

339 SICGVSYVVYGLGNIPPPNKKMKMKVWVSGNATYCALDLFLVMSFARKKLGFG
-----1
389 395
1 match found in sequence:
q9s4d0 : Transporter.
(from "var3spt.pep")
TOIG of: q9s4d0 check: 3300 from: 1 to: 720

ID Q9S4D0 PRELIMINARY; PRT; 720 AA.
AC Q9S4D0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Transporter.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C55;
RX MEDLINE=99346225; PubMed=10417203;
RA Navarathna M.A., Sahi H.G., Tagg J.R.;
RT "Identification of genes encoding two-component ianthyotic production
RT in Staphylococcus aureus C55 and other phage group II S. aureus
RT strains and demonstration of an association with the exfoliative toxin
RT B gene.";
RL Infect. Immun. 67:4268-4271(1999).
DR EMBL: AF147744; AAD47014.1; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001140; ABC_TM_transpt.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR005074; Peptidase_C39.
DR Pfam: PF00064; ABC_membrane_1.
DR Pfam: PF00005; ABC_tran_1.
DR Pfam: PF03412; Peptidase_C39; 1.
DR Prodom: PD000006; ABC_transporter_1.

```

Number of sequence hits saved:

0

DR SMART: SM00382; AAA; 1.
 KW ATP-binding.
 SQ SEQUENCE 720 AA; 81668 MW; EEDAC9DF33C13A24 CRC64;

09S4D0 Length: 720 July 16, 2003 13:46 Type: P Check: 3300 ..
 Found using 'var3' (kam816.key)

654 HVDLSRLKCTKIIVIAHRRFATFNADKIVMDHGEIVEVGAHNELINKNGLYRKLFNAE
 704 710

714 FKKECGV

 1 match found in sequence:
 q9yew0 : Hypothetical protein APE0472.
 (from "var3spt.pep")
 TOTG of: q9yew0 Check: 4517 from: 1 to: 172

ID Q9YEW0 PRELIMINARY; PRT; 172 AA.
 AC Q9YEW0;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein APE0472.
 GN APE0472.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 OC Desulfurococcaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankel A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999)
 DR EMBL; AP000059; BAA79436.1;
 DR InterPro: IPR002716; PIN.
 DR InterPro: IPR006596; PINC.
 DR Pfam: PF01850; PIN; 1.
 DR SMART: SM00670; PIN; 1.
 DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 172 AA; 19704 MW; D735D4BCDD1A83FA CRC64;

Q9YEW0 Length: 172 July 16, 2003 13:46 Type: P Check: 4517 ..
 Found using 'var3' (kam816.key)

114 IALSILKLEAPIWTEDEKALLRASFSNLYVALDTESVENTLHGEPLESIREKLYRKLFRKO
 164 170

-- Search Statistics --

Times: CPU Total Elapsed
 00:00:00.00 00:00:00.00

Number of sequences searched: 10
 Number of sequence hits: 10
 Number of separate matches: 10